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SEARCH REQUEST FORM

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Access DB# 61227

Requester's Full Name: John Yim Examiner #: 69507 Date: 5-22-02
 Art Unit: 1646 Phone Number 308-4008 Serial Number: 09/731657
 Mail Box and Bldg/Room Location: 10B1501 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO: 2 of 09/731657.

STAFF USE ONLY

Contact: Alexandra Wacław
 Technical Info. Specialist
 CM1 6A02 Tel: 308-4491

Searcher Location: _____

Date Searcher Picked Up: 5-23-02

Date Completed: 5-23-02

Searcher Prep & Review Time: 05

Clerical Prep Time: _____

Online Time: 8

Type of Search

NA Sequence (#) _____

AA Sequence (#) 1

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN 1

Dialog _____

Questel/Orbit _____

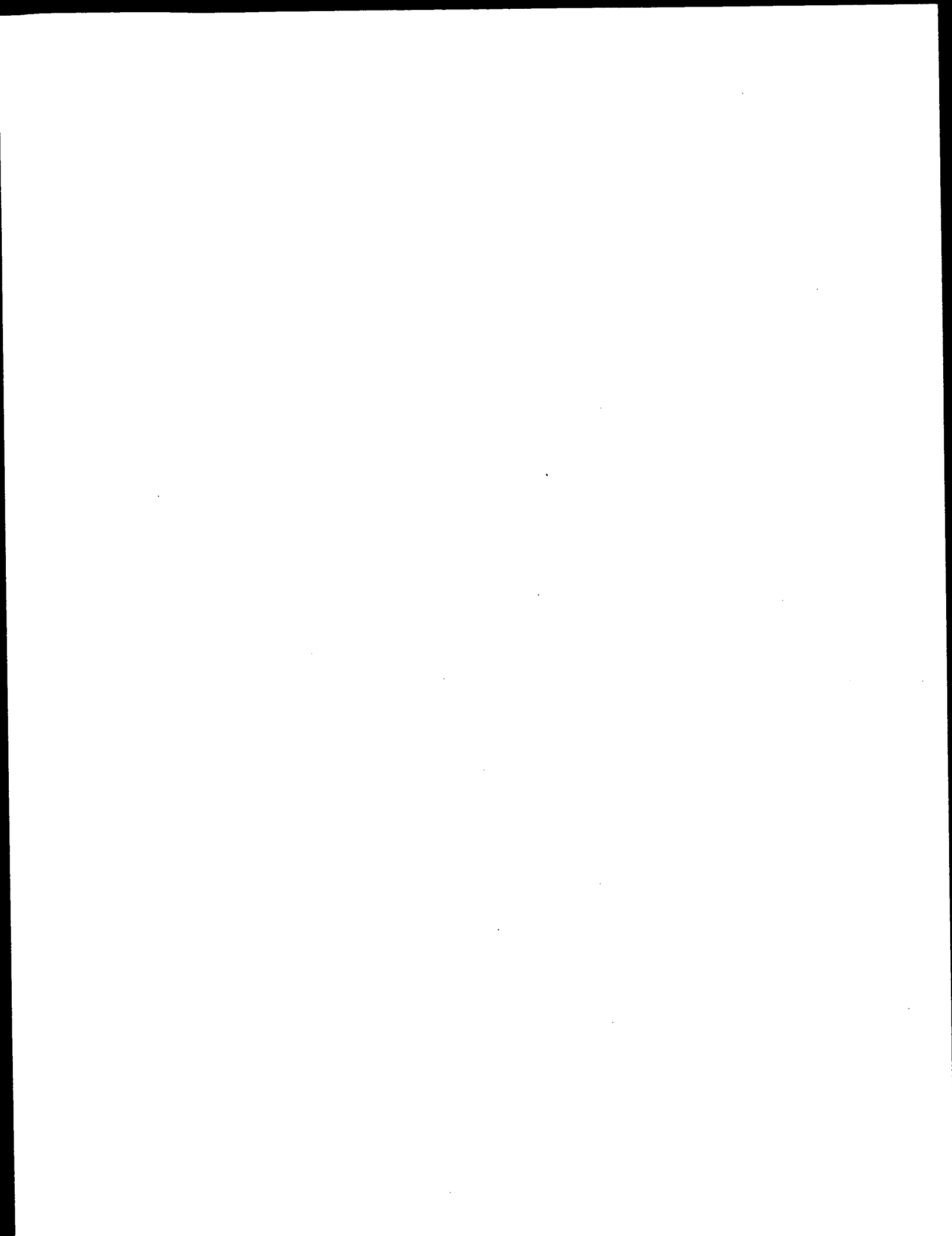
Dr. Link _____

Lexis/Nexis _____

Sequence Systems _____

WWW/Internet _____

Other (specify) Compuizer



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2002, 07:35:15 ; Search time 39.07 Seconds
(without alignments)
2950.975 Million cell updates/sec

Title: US-09-731-657-2

Perfect score: 5352

Sequence: 1 SQPEDASGRCAQRFSTLFSE.....GRMALRRTSKRGLHFIEQM 1038

Scoring table:

BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5352	100.0	1038	18	AAW35903 Human epididymis-s
2	5217.5	97.5	1013	21	AAW01247 Human HE6 receptor
3	1739	32.5	328	22	AAW24057 Human EST encoded
4	1446	27.0	1220	22	AAW00195 Human novel G-prot
5	1446	27.0	1221	22	AAW00191 Human novel G-prot
6	1446	27.0	1221	22	AAW00199 Human novel G-prot
7	1446	27.0	1249	22	AAW00194 Human novel G-prot
8	1446	27.0	1250	22	AAW00190 Human novel G-prot
9	1446	27.0	1250	22	AAW00198 Human novel G-prot
10	1444.5	27.0	1192	22	AAW00712 Human novel G-prot
11	1444.5	27.0	1192	22	AAW00719 Human novel G-prot

12	1444.5	27.0	1193	22	AAU00207 Human novel G-prot
13	1444.5	27.0	1193	22	AAU00716 Human novel G-prot
14	1444.5	27.0	1221	22	AAU00210 Human novel G-prot
15	1444.5	27.0	1222	22	AAU00206 Human novel G-prot
16	1444.5	27.0	1222	22	AAU00715 Human novel G-prot
17	1372.5	25.6	512	22	AAU00203 Human novel G-prot
18	1372.5	25.6	512	22	AAU00203 Human novel G-prot
19	1372.5	25.6	541	22	AAU00202 Human novel G-prot
20	1205	22.5	1111	22	AAU00197 Human novel G-prot
21	1205	22.5	1112	22	AAU00193 Human novel G-prot
22	1205	22.5	1112	22	AAU00201 Human novel G-prot
23	1203.5	22.5	1083	22	AAU00714 Human novel G-prot
24	1203.5	22.5	1084	22	AAU00209 Human novel G-prot
25	1203.5	22.5	1084	22	AAU00718 Human novel G-prot
26	1131.5	21.1	403	22	AAU00205 Human novel G-prot
27	651.5	12.2	687	21	AAU00205 Human novel G-prot
28	630	11.8	687	21	AAU00205 Human novel G-prot
29	629	11.8	687	21	AAU00205 Human novel G-prot
30	625	11.7	687	21	AAU00205 Human novel G-prot
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51	586	10.9	400	22	AAU00205 Human novel G-prot
52	574	10.7	372	22	AAU00205 Human novel G-prot
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57	533	10.0	872	21	AAU00205 Human novel G-prot
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61	530.5	9.9	1114	21	AAU00205 Human novel G-prot
62	530.5	9.9	1177	20	AAU00205 Human novel G-prot
63	530.5	9.9	1177	21	AAU00205 Human novel G-prot
64	530	9.9	1021	21	AAU00205 Human novel G-prot
65	526	9.8	1240	21	AAU00205 Human novel G-prot
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85 501.5 9.4 661 22 AAU18138 Novel human uterin
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87 501.5 9.4 661 22 AAU16983 Human novel secret
88 500.5 9.4 652 21 AAY59300 Human EGPCR polype
89 497 9.3 453 21 AAY94340 Human cell surface
90 495 9.2 190 22 AAM93518 Human polypeptide,
91 494 9.2 2405 21 AAB21292 Human OREX ORF1956
92 494 9.2 2560 22 ABB11404 Human FLAMINGO 1 h
93 494 9.2 2923 22 AAU07054 Human Flamingo pol
94 494 9.2 2956 22 AAU07053 T-cell surface ant
95 491.5 9.2 835 19 AAW48756 Human CD97 protein
96 491.5 9.2 835 21 AAB15728 Human CD97 protein
97 491.5 9.2 359 22 AAE04451 Human novel G-prot
98 487 9.1 217 22 AAG16226 Novel human diagno
99 486.5 9.1 217 22 AAG16226 Human CD97 recepto
100 481.5 9.0 831 21 AAB01248

ALIGNMENTS

RESULT 1

AAW36903

ID AAW36903 standard; Protein: 1038 AA.

XX AC AAW36903;

XX DT 11-MAY-1998 (first entry)

XX DE Human epididymis-specific receptor protein.

XX KW Epididymis-specific receptor protein; transmembrane protein;

XX KW Sperm maturation; male infertility; agonist; antagonist;

XX KW contraception; autoantibody; diagnostic; detection; human.

XX OS Homo sapiens.

XX FH Key . Location/Qualifiers

XX FT Protein 1..1038

XX FT /note= "partial protein sequence"

XX PN DE19617940-A1.

XX PD 30-OCT-1997.

XX PF 29-APR-1996; 96DE-1017940.

XX PR 29-APR-1996; 96DE-1017940.

XX PA (IHFH-) IHF INST HORMON & FORTPFLANZUNGS.

XX PA (HORM-) INST HORMON & FORTPELANZUNGSFORSCHUNG GM.

XX PI Ivell R, Osterhoff C;

XX WPI; 1997-527841/49.

XX DR N-PSDB; AAT97955.

XX PT DNA encoding epididymis-specific receptor protein - useful for

XX PS developing male infertility or contraceptive treatments

XX Claim 1; Page 19-22; 33pp; German.

XX This sequence represents a novel epididymis-specific receptor protein

XX which is a transmembrane protein associated with the epididymis

XX epithelium and is closely connected with sperm maturation. The protein

XX or its derivative or fragments may be useful for detecting autoantibodies

XX in the serum of infertile men and for developing ligands specific for the

XX receptor, e.g. agonists that may stimulate sperm maturation and thus be

XX useful for treating male infertility or antagonists that may be useful

XX for contraception. The antibodies can be used to detect the receptor in

XX vitro or in vivo. Oligonucleotides derived from the DNA sequences can

XX be used as diagnostic probes.

SQ Sequence 1038 AA;

Query Match 100.0%; Score 5352; DB 18; Length 1038;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQPDASGRCAQRFSTLSELAVRMVFSVRQCGHVGRTVEVLLTFKIFLVLCILHVVLT 60

Db 1 sqpedasgrcagrfscliselavrmvsvrqcghvgrtveevlltfkiflvclhvvlt 60

Qy 61 SLEEDTNSLSLPPAKLVSVFAPSNEVETLSLNDVTLSLPSNETEKTKITIVTTFN 120

Db 61 sleedtdnsslppaklvsvsfapsnevettlsldvtlsipsnetektkitivtkfn 120

Qy 121 ASGVKPORNICNLSSICNDSPAFRGEMFYQDKESTVPQNHITNGTLTGVLSELKRS 180

Db 121 asgvkpornicnlsslcnclndspaffrgelmfyqdkestvpqnhlcnltgvlslselkrs 180

Qy 181 ELNKTLOTSETYFIMCATAEAQSTLNCTFTIKLNTMTNACAATAALERVKIRMEHCCC 240

Db 181 elnktlotsetyfimcataeaqstlnctftiklntmtnacaataalervkirmehccc 240

Qy 241 SVRIPCSPSEELGKLQCDLQDPVCLADHPGPPFPSSSSQSIPIVPRATVLSQVPKATSF 300

Db 241 svripccspseelgklqcdlqdpivcladhpgrppfssssqsiipivpratvlsqvpkatsf 300

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Db 361 pvkafssptvsapanvnttsappvqtdivntssisdlenovlqmerkalsglepnlag 420

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Db 421 eminqvsrllhspddmlaplaqrllkvddigqlnfnsttisltspslalatavirvnass 480

Qy 481 FNTTFVAQDPANLQVSLETQAPENSIGTITLPSLNNLPAHDMELASRVQNFETPA 540

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Db 781 nyglgsygfppngspddfcwlnnavfiyvtvgvfcvifllnvsmfivvvlqlcrlikkk 840

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Db 841 qlgaqrktsiqdlrsiagltfllgitwgfaffagvnpvntfmylfaifnloggffify 900

Qy 901 CVAKENVRKQWRYLCCGKRLAENSWSKATNGLKQTVNQGVSSSSNSLQSSNSN 960

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Db 961 sttlvvnndcsvgasngngasternvgsfvqngdvclhdfgkqmfnekedscngkr 1020

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OM protein - protein search, using sw model

Run on: May 23, 2002, 07:35:20 ; Search time 17.89 seconds
(without alignments)
1417.203 Million cell updates/sec

Title: US-09-731-657-2
Perfect score: 5352
Sequence: 1 SQPDASGRCAQRFSTLFE.....GRMALRRTSKRGLHFIEQM 1038

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	463	8.7	344	3	US-09-110-116-4
5	438	8.2	886	3	US-09-110-116-3
6	411.5	7.7	1052	2	US-08-852-806-2
7	411.5	7.7	1052	3	US-09-163-669-2
8	367.5	6.9	884	2	US-08-465-976A-2
9	367.5	6.9	884	2	US-08-982-412-2
10	290	5.4	240	4	US-09-370-098-5
11	286	5.3	235	4	US-09-370-098-6
12	245.5	4.6	231	4	US-09-370-098-4
13	240.5	4.5	1324	2	US-08-811-897A-56
14	233	4.4	448	2	US-08-811-897A-18
15	233	4.4	448	2	US-08-855-213-18
16	233	4.4	467	2	US-08-811-897A-19
17	233	4.4	467	2	US-08-855-213-19
18	231.5	4.3	448	2	US-08-811-897A-16
19	231.5	4.3	448	2	US-08-855-213-16
20	231.5	4.3	485	2	US-08-811-897A-17
21	231.5	4.3	485	2	US-08-855-213-17
22	231	4.3	476	2	US-08-811-897A-20
23	231	4.3	476	2	US-08-855-213-20
24	231	4.3	495	2	US-08-811-897A-21
25	231	4.3	495	2	US-08-855-213-21
26	230	4.3	415	1	US-08-110-286A-6
27	230	4.3	415	4	US-08-981-189B-10

28	228.5	4.3	476	2	US-08-811-897A-14	Sequence 14, Appl
29	228.5	4.3	476	2	US-08-855-213-14	Sequence 14, Appl
30	228.5	4.3	513	2	US-08-811-897A-15	Sequence 15, Appl
31	228.5	4.3	513	2	US-08-855-213-15	Sequence 15, Appl
32	227.5	4.3	448	2	US-08-811-897A-22	Sequence 22, Appl
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34	227.5	4.3	525	2	US-08-811-897A-23	Sequence 23, Appl
35	227.5	4.3	525	2	US-08-855-213-23	Sequence 23, Appl
36	226.5	4.2	376	2	US-08-465-976A-3	Sequence 3, Appl
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38	226	4.2	415	1	US-08-110-286A-2	Sequence 2, Appl
39	225	4.2	475	2	US-08-811-897A-26	Sequence 26, Appl
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43	224.5	4.2	476	2	US-08-811-897A-24	Sequence 24, Appl
44	224.5	4.2	476	2	US-08-855-213-24	Sequence 24, Appl
45	224.5	4.2	553	2	US-08-811-897A-25	Sequence 25, Appl
46	224.5	4.2	553	2	US-08-855-213-25	Sequence 25, Appl
47	215.5	4.0	431	4	US-08-981-189B-13	Sequence 13, Appl
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51	214.5	4.0	553	2	US-08-811-897A-29	Sequence 29, Appl
52	214.5	4.0	553	2	US-08-855-213-29	Sequence 29, Appl
53	209	3.9	411	1	US-08-381-433A-4	Sequence 4, Appl
54	209	3.9	411	4	US-08-981-189B-12	Sequence 12, Appl
55	208	3.9	431	4	US-08-981-189B-11	Sequence 11, Appl
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63	188.5	3.5	437	4	US-09-208-394-2	Sequence 2, Appl
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67	185	3.5	585	1	US-08-142-439A-6	Sequence 6, Appl
68	185	3.5	585	2	US-08-142-551B-125	Sequence 125, Appl
69	185	3.5	585	2	US-08-869-477-6	Sequence 6, Appl
70	185	3.5	585	2	US-08-468-249A-19	Sequence 19, Appl
71	183	3.4	593	2	US-08-468-249A-21	Sequence 21, Appl
72	181	3.4	591	2	US-08-468-249A-20	Sequence 20, Appl
73	180	3.4	485	1	US-08-453-956-15	Sequence 15, Appl
74	180	3.4	485	2	US-08-086-631-15	Sequence 15, Appl
75	180	3.4	485	2	US-08-452-930-15	Sequence 15, Appl
76	180	3.4	485	5	PCT-US93-08174-15	Sequence 15, Appl
77	179	3.3	458	1	US-08-112-817C-2	Sequence 2, Appl
78	177.5	3.3	477	1	US-08-453-742-27	Sequence 27, Appl
79	177.5	3.3	477	1	US-08-454-464-27	Sequence 27, Appl
80	177.5	3.3	477	1	US-08-453-222-27	Sequence 27, Appl
81	177.5	3.3	477	1	US-08-452-802-27	Sequence 27, Appl
82	177.5	3.3	541	3	US-08-468-011A-2	Sequence 2, Appl
83	177.5	3.3	541	5	US-09-236-468A-2	Sequence 2, Appl
84	177.5	3.3	541	5	PCT-US95-07085-2	Sequence 2, Appl
85	176	3.3	482	1	US-07-792-885A-1	Sequence 1, Appl
86	176	3.3	482	2	US-08-142-439A-7	Sequence 7, Appl
87	176	3.3	482	2	US-08-869-477-7	Sequence 7, Appl
88	175	3.3	474	1	US-08-453-742-2	Sequence 2, Appl
89	175	3.3	474	1	US-08-454-464-2	Sequence 2, Appl
90	175	3.3	474	1	US-08-453-222-2	Sequence 2, Appl
91	175	3.3	474	1	US-08-452-802-2	Sequence 2, Appl
92	174.5	3.3	474	4	US-09-370-098-2	Sequence 2, Appl
93	171.5	3.2	294	1	US-08-142-439A-4	Sequence 4, Appl
94	171.5	3.2	294	2	US-08-869-477-4	Sequence 4, Appl
95	171	3.2	431	2	US-08-538-816A-9	Sequence 9, Appl
96	171	3.2	431	2	US-09-076-651-9	Sequence 9, Appl
97	171	3.2	431	4	US-09-208-394-9	Sequence 9, Appl
98	171	3.2	438	2	US-08-538-816A-1	Sequence 1, Appl
99	171	3.2	438	2	US-09-076-651-1	Sequence 1, Appl
100	171	3.2	438	4	US-09-208-394-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-956-322-4
; Sequence 4, Application US/08956322
; Patent No. 6277977
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: MAO, JOYCE
; TITLE OF INVENTION: CDNA CLONE HAP0167 THAT ENCODES
; TITLE OF INVENTION: A HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956.322
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/049,329
; FILING DATE: 11-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70075
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 521 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-322-4

Query Match 9.4%; Score 501.5; DB 4; Length 521;
Best Local Similarity 28.7%; Pred. No. 5.3e-32;
Matches 155; Conservative 95; Mismatches 197; Indels 93; Gaps 19;

QY 398 LENQVL-QMEKALSLGSLFNPAGEMINOVSRLLHSPDMLAPLAQRLLKVVDIDIGLQLN 456
Db 12 LTNQVLRTGREGQISSTATTILRDVESKVLTAIXDPE-----QKVLKIQND----- 59
QY 457 FSNITISLTPSLALAIRVNASSFNFTTVAODPANLQVSL-----ETQAP 503
Db 60 -----SVAIQATIDNGSEERKT-----FNLNVQMNSMDIRCSDFIIQGDTPG 103
QY 504 ENSIGTITLPSSLMNPLPAHDMELASRVQFNFTETPALFODPSSLNLSLISYVSSSVAN 563
Db 104 -SAIAFISYS-----LGLIINATFEE-----EMDKKDQVYLNQVYSAAGP 145
QY 564 LTVRNLTNVTYTLKHINPSQDELTVRCVFDLGRNGRGG-WSDNGSCVKDRRLNETIC 622
Db 146 KRVSLKSVTLTFQHKVKTPTSTKKFVCVW---KSTGQGSQWSRDGCFLLIHVNKSHITMC 202
QY 623 TCSHLTSGVLLDLSTSVLPAQMALTFTTYICGGLSSIFLSVTLTYIAFAEKIRRDYP 682

Db 203 NCSHLSFAVLMAITSQEDP-----VLTIVTVGLSVSLCLLAALTELLCKAIQNTST 258
QY 683 SKILIQCAALLNLVFLDLSWIALYKMGCLICISAVAFELHYELLYSFTWMGLEAFHMYL 742
Db 259 S-LHLQLSLCLFLAHLFLVG--IDRTEPKVLCISIIAGALHYLYLAFTWMLLEGVHLFL 315
QY 743 AL--VKFNTVIRKYILKFCI--VGMGVPAVVVTIITLITSPDNYGLSGYKGFNPGSPDDF 798
Db 316 TARNLTVVNYSSINRLMKWIMEFVGVGVPATVVAISAASWPHLYGTA-----DR 364
QY 799 CWINNNAVYITVVGVCYFVFLNYSMFIVLVOLCRKKKQKOLGAQRKTSIQDLRSIA- 857
Db 365 CWLHLDQGFMSFLGVCFAIFSANLVLFLVFWILKR--KLSSINSEVST-IQNRMLAF 421
QY 858 ---GLTFLLGITWGAFFAWGVNVVTFMYLFAFNLTLOGFFIFFYCVAKENVRKQWRY 914
Db 422 KATAQLFILGCTWCLGLLOVGPAQVMAYLFTIINSLOGFFIFLVYCLLSQOVQKQKXW 481

RESULT 2
US-08-956-322-2
; Sequence 2, Application US/08956322
; Patent No. 6277977
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: MAO, JOYCE
; TITLE OF INVENTION: CDNA CLONE HAP0167 THAT ENCODES
; TITLE OF INVENTION: A HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956.322
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/049,329
; FILING DATE: 11-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70075
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 652 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-322-2

Query Match 9.4%; Score 501.5; DB 4; Length 652;
Best Local Similarity 28.7%; Pred. No. 7.6e-32;
Matches 155; Conservative 95; Mismatches 197; Indels 93; Gaps 19;

QY 398 LENQVL-QMEKALSLGSLFNPAGEMINOVSRLLHSPDMLAPLAQRLLKVVDIDIGLQLN 456
Db 12 LTNQVLRTGREGQISSTATTILRDVESKVLTAIXDPE-----QKVLKIQND----- 59
QY 457 FSNITISLTPSLALAIRVNASSFNFTTVAODPANLQVSL-----ETQAP 503
Db 60 -----SVAIQATIDNGSEERKT-----FNLNVQMNSMDIRCSDFIIQGDTPG 103
QY 504 ENSIGTITLPSSLMNPLPAHDMELASRVQFNFTETPALFODPSSLNLSLISYVSSSVAN 563
Db 104 -SAIAFISYS-----LGLIINATFEE-----EMDKKDQVYLNQVYSAAGP 145
QY 564 LTVRNLTNVTYTLKHINPSQDELTVRCVFDLGRNGRGG-WSDNGSCVKDRRLNETIC 622
Db 146 KRVSLKSVTLTFQHKVKTPTSTKKFVCVW---KSTGQGSQWSRDGCFLLIHVNKSHITMC 202
QY 623 TCSHLTSGVLLDLSTSVLPAQMALTFTTYICGGLSSIFLSVTLTYIAFAEKIRRDYP 682

Db 961 stlllvndcsvhasngnasterngvsfsvqngdvclhdfgkghmfnekedscngkgr 1020

Qy 1021 MALRRTSKRGLHFIQOM 1038

Db 1021 malrtrskrgslhfiqom 1038

RESULT 2

AA01247

ID AAB01247 standard; Protein; 1013 AA.

AC AAB01247;

DT 03-OCT-2000 (first entry)

DE Human HE6 receptor.

XX

KW Human; HE6 receptor; zsig56; seven transmembrane domain receptor; hypotensive; antigout; cytostatic; antiinflammatory; ion homeostasis; cardiant; neurotransmitter; neuroprotective; antiparkinsonian; cerebrotective; nootropic; neuroleptic; tranquiliser; antiarthritic; reproductive; signal transduction activator; bone disease; hypertension; renal failure; heart failure; hyperthyroidism; hyperparathyroidism; carcinoma; sarcoidosis; pancreatitis; stress; high blood pressure; immune depression; periodontal disease; neurodegenerative disease; multiple sclerosis; Alzheimer's disease; Parkinson's disease; schizophrenia; manic depression; stroke; rheumatoid arthritis; male fertility; spermatogenesis stimulation; pregnancy regulation; prostate cancer.

KW OS Homo sapiens.

XX

PN WQ20003473-A2.

PD 15-JUN-2000.

XX

PF 02-DEC-1999; 99WO-US28492.

XX

PR 10-DEC-1998; 98US-0208691.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

PI Sheppard PO, Ellsworth JL;

XX

DR WPI; 2000-442164/38.

XX

PT Novel G-protein coupled receptor zsig56 useful for treating hypertension, hyper and hypothyroidism, inflammation, gout, carcinoma, pancreatitis, Alzheimer's disease and Parkinson's disease, renal and heart failure -

XX

PS Disclosure; Fig 1; 121pp; English.

XX

CC The present sequence is the human HE6 receptor, which shows homology to a seven transmembrane domain receptor designated zsig56. The full length nucleotide sequence was obtained from a human retina library. zsig56 polypeptides, nucleic acid, agonists and/or antagonists may be used to treat a wide range of disorders including certain bone diseases, hypertension, renal failure, gout, congestive heart failure, hyperthyroidism, hyperparathyroidism, certain carcinomas, sarcoidosis and pancreatitis. They can be used to treat disorders associated with changes in ion or electrolyte homeostasis, and stress induced disorders such as high blood pressure, heart failure, immune depression and periodontal disease. They may be used to treat neurodegenerative diseases, including multiple sclerosis, Alzheimer's disease and Parkinson's disease, schizophrenia and manic depression, and to repair nerve tissue following damage due to strokes and brain and spinal injuries. Inflammatory disorders such as rheumatoid arthritis can also be treated. zsig56 is expressed in tissues associated with reproduction, i.e. the testis, prostate and placenta, and may be used to treat male fertility by stimulating spermatogenesis and to regulate gestation and birth. zsig56 may be useful as a marker or therapeutic agent in the treatment of prostate cancer.

XX	Sequence	1013 AA;	Query Match	97.5%;	Score 5217.5;	DB 21;	Length 1013;
QQ			Best Local Similarity	99.9%;	Pred. No. 0;		
			Matches 1013;	Conservative	0;	Mismatches	0;
						Indels	1;
						Gaps	1;
QY	25	MVPSVRCQGHVGRTEVLLTFKIFLVICLHVLTSLSEEDTNSLSLSPPAKLSVVSFA	84				
DB	1	mvfsvrgcghvgrteevlltfkiflviclhvltslseedtndsslsppaklsvvsfa	60				
QY	85	PSSNEVETTSINDVTLSLLPSNETKTIIVKTFENASGVKPPORNICNLSSICNDSAFPR	144				
DB	61	psnevettsindvtlsllpsnetektktivkfnsagvkkpqrnicnlssicndsafr	120				
QY	145	GEIMFYDKESTVPQNOHITNGTLTGVLSELKRSSELNKTLOTSETYFFIMCATAEAGS	204				
DB	121	geimfydkestvpqnhitngtlgtvlsisekrseinkltlqitsetyfincataeags	180				
QY	205	TLNCTFTIKLNTNMACAAATAALERVKIRMEHCCSVRIPCSPSPBELGKLQCDLQDPI	264				
DB	181	t-nctftiklntnmacaataalervkirmehccsvripccspspbelgklqcdlqdpi	239				
QY	265	VCLADHPRGPPFSSQSIPVPRATVLSQVPKATSFAPPPDYSPVTHVPSPIGFIQPLS	324				
DB	240	vcladhprgppfssqsipvpratvlsqvpkatsfaepdyspvthvpspiqipls	299				
QY	325	POPSAPIASSPAIDMPPQSETISSPMQTHVSGPPPVKASFSSPTVSAPANVNTTSAPP	384				
DB	300	popsapiasspa idmppqsetisspmqthvsgtpppvkasfsptvsapanvnttsapp	359				
QY	385	VGTDIVNTSSISDLENQVLMKALSGLEPNLAGEMINQVSRLLHSPDMLAPLAORL	444				
DB	360	vgtdivntssisdlenqvlmekalslgslepnlageninqvsrllhspdmleplagrl	419				
QY	445	LKVDDIGLQNFNTTISLTSPSLALAVIRVNASSFNTTFFAQDDPANLVSLQTAPE	504				
DB	420	lkvddiglqlnfnttisltspslalavirvnassfnttffvaqddpanlvslqetqpe	479				
QY	505	NSIGITTLPSLLMNNLPAHDMELASRVQNFETPALFQDPSLENLSISVIVSSVANL	564				
DB	480	nsigitlpsllmnnlpahd melasrvqnfetpal fqdpslenlsisvissvanl	539				
QY	565	TVRNLTNRVTVTLKHINPSQDELTVRCVFDLGRNGRGWSNDGSCVKDRRLNETICTC	624				
DB	540	tvrnltnrvtvltkhinpsqdel tvrcvfdlgrngrgwsgndgscvkdrrlnetictc	599				
QY	625	SHLTSEGVLLDLSRTSVLPAQMMALFTIYIGCGLSIFISVTLTVYIAFEKIRRDYPSK	684				
DB	600	shltsegvllldlsrtsvlpaqmmaltfiyigcglssifisvltlvtlyiafekirrdypsk	659				
QY	685	ILIQCALLLNVLNLFLLDSWIALYKMOGLCISVAVFLHYVFLVFTFMGLEAFHMYIAL	744				
DB	660	liqlcaalllnvllfldswialykmqglcisvavflhyflvftfmgleafhmyial	719				
QY	745	VKVFNTYIRKYILKFCIVGWGPVAVVVTIILTISPONVGLSGYKFPNGSPDDFCWINNN	804				
DB	720	vkvfntyirkyilkcivgwgpavvvvtiiltispdnyglsgykgfngspddfcwinnn	779				
QY	805	AVFYITVGVYFCVIFLLNVSMFIVLVQLCRKKKQKOLGAQRKTSIODLSRIAGLFTLLG	864				
DB	780	avfyitvgyfcvifllnvsmfivlvqlcrkkkqlgaqrktsiodlsriagltfllg	839				
QY	865	ITWGAFFAWGPVNVTFMYLFAIFNTLOGFFFIYFCVAKENVRKOWRRYLCGCKLRRAE	924				
DB	840	itwgaaffawgpvnvtfmylfaifntlqgffifcyvakenvrkwrrylcogcklrcae	899				
QY	925	NSDWSKTATNGLKKTQVNOGVSSSSNSLQSSNSTNTTLLVNNDCSVHASGNGNASTER	984				
DB	900	nsdwsktatnglkkktvngvgvssssnslqssnsnttllvnndcsvhasngnaster	959				
QY	985	NGVSFSVQNGDVCLHDFGKGHMFNEKEDSCNGKGRNALRRTSKRGLHFIQOM	1038				

891 LOGFFIIFCYVAKENVRKOWRRYLCCGKRLAENSDWKSATNGLKQTVNOGVSSSN 950
181 lqgffifficyvakenvrkqrrylccgkrlaensdsktatnglkkqtvnqgvsssn 240
951 SLOSSNSTSTLLVNNDCSVHASGNGNASTERNVGSFVSQNGDVCCLHDTGCKQHMFNE 1010
241 slqssnststllvnnncsvhasngnasternvgsfvsqngdvcclhdtgkqhmfne 300
1011 KEDSCNGKGRMALRRTSKRGSILHFIETQM 1038
301 kedsncngkgrmalrrtskrgrsilhfielqgm 328

RESULT 4
AAU00195
ID AAU00195 standard; Protein; 1220 AA.
XX
AC AAU00195;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human novel G-protein coupled receptor, NGPCR#6.
XX
KW Human; novel G-protein coupled receptor; NGPCR; antagonist;
KW agonist; diabetes; obesity; atherosclerosis; heart disease;
KW abnormal blood pressure; cancer.
XX
OS Homo sapiens.
XX
PN WO200118207-A1.
XX
PD 15-MAR-2001.
XX
PF 08-SEP-2000; 2000WO-US24591.
XX
PR 10-SEP-1999; 99US-0153366.
PR 15-NOV-1999; 99US-0165510.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;
PI Sands AT;
XX
DR WPI: 2001-191773/19.
DR N-PSDB; AAS00115.
XX
PT New nucleic acids encoding human G-protein coupled receptors, useful as
PT a therapeutic target for diabetes, obesity, atherosclerosis, heart
PT disease and cancer -
XX
PS Disclosure; Page 78-80; 149pp; English.
XX
CC The sequence represents a Human novel G-protein coupled receptor (NGPCR).
CC The NGPCRs are members of the 7 transmembrane domain class of
CC receptors. The NGPCR proteins of the invention, polynucleotides encoding
CC them and (ant)agonists of the NGPCRs are useful for the treatment
CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart
CC disease, abnormal blood pressure, cancer and any associated symptoms.
XX
SQ Sequence 1220 AA;

Query Match 27.0%; Score 1446; DB 22; Length 1220;
Best Local Similarity 35.4%; Pred. No. 4.4e-98;
Matches 365; Conservative 183; Mismatches 330; Indels 154; Gaps 35;

QY 68 NSSLSPPAKLSVVSFAPSNE---VETTSNDVTLSPNSNETKTKITIVKTFNAGSV 124
Db 233 nnaal---pvkededifaesfeqlcvwnslsglgnvkrnyetvpodstisk-----v 283
QY 125 KPQRNCTNLSICNDSAFFRGEIMFYQDKESTVPQNOHITNGTLTGVLSELKPSLNK 184
Db 284 ibpgnklllgnsnqneivslkgdi-----ynfrlwnftmaki-lsnlscnvkgn 331

960 ngvsvsqngdvcclhdtgkqhmfnekedscngkgrmalrrtskrgrsilhfielqgm 1013

RESULT 3
AAM24057
ID AAM24057 standard; Protein; 328 AA.
XX
AC AAM24057;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST encoded protein SEQ ID NO: 1582.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI: 2001-476164/51.
DR N-PSDB; AAH98716.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 20; Page 1081-1082; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX
SQ Sequence 328 AA;

Query Match 32.5%; Score 1739; DB 22; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.3e-120;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 711 MGLGISVAVFLHYFLVSVFTWGLEAFHMYLALVKVFNTYIRKYILKFCIVGWGPVAV 770
Db 1 mglgisvavflhyflvsvftwmgleaflhmylalkvkvntyirkyilkkfcivgwgvpav 60
QY 771 VTILITISPDNNGLSYCKFPNGSPDDFCWNNNAVYITVVGVCYFVFLNYSMEIWL 830
Db 61 vtilitispdnnglsyckfpngspddfcwinnnavyitcvgyfcvflnysmfivl 120
QY 831 VOLCRIRKKKQLGAQRKTSIODLRSTAGITFLIGITWGEFAFFWAGPVPVNTFMYLFAFNT 890
Db 121 vqlcrirkkkqlgaqrktsiqdlrsiagitfligitwgfaffwagpvpvntfmylfaifnt 180

QY 407 KALSU-GSLEPNLAGEMINQVSRLLHSPDMLAPLAQRLLKVVDDIGLQNFSTT-LSL 464
 Db 615 rivnkeeniditlgtlmmifslssdsdlessealktidelfakidlnstshvni 674
 QY 465 TSPSLALAVIRVNASSFTTFFVAQDPAN-...LQVSLTQAPENSIGITITLPSLLMNL 520
 Db 675 ttrnlalsvslpgtnaisnfsiglpnnesyfmdfes-gqvdpasvilpplnlenl 733
 QY 521 PAHDMELASRVQNFETFPALFQDPSLENLSLISYVSSSVANLTVRNLTRNVTVLKHI 580
 Db 734 spedsvlvrragqtfknktglfdvgpqrktlvsvymacsignitignkdpvgikikt 793
 QY 581 NPSQDELTVRCVFDLGRNGRGWSNDGC-SVKDRRLNETICTCSHLTSGVLLDLSRT 639
 Db 794 rtqevhpi-cafwdlnknksfggwntsgcvahrdsdasetvclcnhthfvgvmdlprs 852
 QY 640 -SVLPAQ-MMALTFITYIGCLSSIFLSVTLVYIAFEKIRRDYPSKILFOLCAALLLN 697
 Db 853 asqldarntkvltfisyigcisaifsaatlityvafeklrdrdpskilmlnstallfln 912
 QY 598 LVFLDLSHIALYKMGICISVAVFHYFLVLLVFTWNGLEAFHMYLALVKVFNTRYIRKYL 757
 Db 913 lflldgwitsfnvdglciavavllhffllatftwmgleahmyialvkvntvrryil 972
 QY 758 KFCIVGCVPAVWVTIILTISPDN--YGLGSYKFPNGSPDDFCWINNNNAFFYITVVGIF 815
 Db 973 kfcigwglpalvsvvlasrnnnnyvkesyvk---ekgdefcwigdpvifvycagf 1029
 QY 816 CVIFLLNVSMFIVLVQICRIKKKOLGAQRKTSIODLSRIAGLTLLGTWGFAPFANG 875
 Db 1030 gvmfflniamfivmvqicgrngkrnrlreevlnrlsvvsltflgntwgfaffaw 1089
 QY 876 PVNVTEMVLEAFNTLOGFFIFIEYCVAKENVRKQWRYLCCGKRLAENSDSKTATNG 935
 Db 1090 pinlpfmylfafnsigqlffifhcamkenvqkqrhlccgfrfladnswsktatni 1149
 QY 936 LKQTVNGVSSSSSLQSSS-----NSTNTLLLVNNDSCSVHAGSNGNASTERNVSVF 989
 Db 1150 ikkasdnlgkslssssignsnyltskskssttyfkrn-----shtdnvsyeh---sf 1200
 QY 990 SVQNGDV--CLH 999
 Db 1201 n-kagslrqcfh 1211

RESULT 6

AAU00199 standard; Protein; 1221 AA..

AAU00199;

12-SEP-2001 (first entry)

Human novel G-protein coupled receptor, NGPCR#10.

Human; novel G-protein coupled receptor; NGPCR; antagonist; agonist; diabetes; obesity; atherosclerosis; heart disease; abnormal blood pressure; cancer.

Homo sapiens.

WO200118207-A1.

15-MAR-2001.

08-SEP-2000; 2000WO-US24591.

10-SEP-1999; 99US-0153366.

15-NOV-1999; 99US-0165510.

(LEXI-) LEXICON GENETICS INC.

PI Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;
 Sands AT;
 XX WPI: 2001-191773/19.
 DR N-PSDB: AAS00119.
 XX New nucleic acids encoding human G-protein coupled receptors, useful as
 PT a therapeutic target for diabetes, obesity, atherosclerosis, heart
 PT disease and cancer -
 XX Disclosure; Page 91-93; 149pp; English.
 XX The sequence represents a Human novel G-protein coupled receptor (NGPCR).
 CC The NGPCRs are members of the 7 transmembrane domain class of
 CC receptors. The NGPCR proteins of the invention, polynucleotides encoding
 CC them and (ant)agonists of the NGPCRs are useful for the treatment
 CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart
 CC disease, abnormal blood pressure, cancer and any associated symptoms.
 XX Sequence 1221 AA;

Query Match 27.0%; Score 1446; DB 22; Length 1221;
 Best Local Similarity 35.4%; Pred. No. 4.4e-98;
 Matches 365; Conservative 183; Mismatches 330; Indels 154; Gaps 35;

QY 68 NSSLSPPPAKLVSVPAPSSNE---VETSLNDVTLSSLPSNETETKTIIVKTFNSGV 124
 Db 234 mnal---pvkekeidiaefedqiclvwnslsgisgvnfrknyetvpcdstisk-----v 284
 QY 125 KPORNICNLSSICNSGAPFRGETMFQYDKRESTVPQNHITNGTLGVLSLSELKRSELNK 184
 Db 285 lpgngkliligsnqneivslkgdi-----ynfrlwnftmaki-lanlsncvkgk 332
 QY 185 TLQTLSETVFIMCATAEAOSTLNC-TFTIKLNT-MNACAAIAALERVKIRPMEHCCCV 242
 Db 333 vvdgndfwnlpnlakaesnlscgsylplpaaelascadigtl-----cqvav 382
 QY 243 RTPCPSSPEELKQLCQDLPVCLADHPR--GPPFSSS---QIPVVPVATVLSQVPR- 296
 Db 383 nspsttpvtvtnm-----pvtnrldkgrndgilyrisvviqnlilrhpevkvsqvaev 436
 QY 297 ATSFAPDPDYSPVTHNV-----PSPIGEIPLSPOP----- 327
 Db 437 lnstfgwnvtyvvnvnisfhlsagedkikvksledeprlvllvallynatntnlegki 496
 QY 328 --SAPIASSPAIDMPPQSETIS-----SPMQTHVSGTTPPVKASF 366
 Db 497 lqgklknnesidegirlhtvnrqighclameepkgyvpsiqpsev--lpcdpkpgf 554
 QY 367 S-----SPTVS--APANVT--TSAPPVQTDVNTS-----SISLENOVLQME 406
 Db 555 sasricfynatnplvtvvgpvdiscnlikeanvanqilnitadggnitsanitniveqvk 614
 QY 407 KALSU-GSLEPNLAGEMINQVSRLLHSPDMLAPLAQRLLKVVDDIGLQNFSTT-LSL 464
 Db 615 rivnkeeniditlgtlmmifslssdsdlessealktidelfakidlnstshvni 674
 QY 465 TSPSLALAVIRVNASSFTTFFVAQDPAN-...LQVSLTQAPENSIGITITLPSLLMNL 520
 Db 675 ttrnlalsvslpgtnaisnfsiglpnnesyfmdfes-gqvdpasvilpplnlenl 733
 QY 521 PAHDMELASRVQNFETFPALFQDPSLENLSLISYVSSSVANLTVRNLTRNVTVLKHI 580
 Db 734 spedsvlvrragqtfknktglfdvgpqrktlvsvymacsignitignkdpvgikikt 793
 QY 581 NPSQDELTVRCVFDLGRNGRGWSNDGC-SVKDRRLNETICTCSHLTSGVLLDLSRT 639
 Db 794 rtqevhpi-cafwdlnknksfggwntsgcvahrdsdasetvclcnhthfvgvmdlprs 852
 QY 640 -SVLPAQ-MMALTFITYIGCLSSIFLSVTLVYIAFEKIRRDYPSKILFOLCAALLLN 697
 Db 853 asqldarntkvltfisyigcisaifsaatlityvafeklrdrdpskilmlnstallfln 912

Db 332 vvdwqndfwnipnlalkaesnlscgysylipipaaelascadlgticqdgilryisvviq- 390
 Qy 152 DKESTVPQNHITNGTLTGVLSELKRS-----LNKTLQTLSETYFTMCATAEAQSTL 206
 Db 391 -----nllrhpevkqskvaewlnstfgwnyvtvyv-----v 422
 Qy 207 NCTFTIKLNTMNACAAIAALERKIRPMEHCCSVRIPCSPPEELGKL----- 256
 Db 423 nlsfhls-----agedkikvk-----rsledeprlwallvyna 457
 Qy 257 --QCLODQDIVLADHPRGPPFSSQSIPVPRATVLS--QVPKATSAEPDPYSPVTHN 312
 Db 458 tnntnlegkili-----qqkllknesldegrlrhtvnvrglghclameepkgy-----y 506
 Qy 313 VPSPIGEIQP---LSPQPSAPIASSPAIDMPPQSETISSPMPQTHVSGTPPPVKAFSSP 369
 Db 507 wps-----lqpsyvlpcpdkpgfsasri-----cfynatnplv----- 540
 Qy 370 TVSAPANVNT--TSAPPVQTDIVNTS-----SISDLENQVLOMEKALSL-GSLEPNLAG 420
 Db 541 tywgpvdisclickeanevanqilntadgqnltsantivneqvkriynkeeniditlgs 600
 Qy 421 EMINQVSRLLHSPDMLAPLAQRLKLVVDDIGLOLNFSTNT--ISLTSPLALAVIRVNAS 479
 Db 601 tlmnifsnlssdsdlsesaealktdelafklidlnstshvntitnlnalsvslpg 660
 Qy 480 SPNTTTFVAQDPAN---LQVSLTOAPENSIGTITLPSLSLMMNLPAMDMLASRVQFNF 535
 Db 661 tnaifnsglpennesyfgmdfes-gvqdpiasvlpnlnlenlspedsvlvrraqftf 719
 Qy 536 FETPALFQDPSLENLSIYSSIVSSVANLTVRNITRNVTVLKHNPSODELTVRGVFWD 595
 Db 720 fktglfgdvgprkltvsvvmcasignitqilnkdpvqikikhrtdqevhhpi-cafed 778
 Qy 596 LGRNGRGQWSDNGC-SVKDRRLNETICTCSHLTSFGVLLDLSRI-SVLPAQ-MMALTFI 652
 Db 779 lnkksfggwntsgcvahrdsdasetvclcnhfhgfvldmldrpsasqldarntkvlfti 838
 Qy 653 TYVIGCLSSIFLSTVLTVYAFKIRDRDPSKILIQICAAALLLNLVFLDLSWIALYKMQ 712
 Db 839 syigcgisalfsaatltyvafeklrdrdpskilmnltallfllldgwltsfnvd 898
 Qy 713 GLCISVAVFLHFLVSYFTWGLAEAFHMYLALVKVFNTYIRKYILKFCIVGWGVPAVVVT 772
 Db 899 glciavavllhflfatftwmgileahmyialkvfntyirryilkfcligwlpalvvs 958
 Qy 773 ILTITSPDN--YCLGSYGKFPNGSPDDFCWINNNAVFYITVVGVFCVIFLLNVSMFIVL 830
 Db 959 vvlarnnnevgykesygk---ekgdefcwiqdpvifvtcagyfgvmfflniamfivm 1015
 Qy 831 VOLCRKIKKKOLGAORKTSTQDLRSIAGTLFLLGITWGFAPFAMGPNVNTFMFLFAFENT 890
 Db 1016 vqicgrngkrnsrtlrreevlnrsvslftlgtmtwgfaffawgplnlpmylfsifns 1075
 Qy 891 LOGFTIFIFCYAKENVRQWRRYLCCGKLRLAENSWSKATNGLKKQTVNQGVSSSN 950
 Db 1076 lqglflifhcamkenvgqwrthlccgrflrldadswsktatnlkssdnlgsllss 1135
 Qy 951 SLQSSS-----NSTNSTVLLVNDCSVHASGNAGNASTERNGVSFVSQNGDV--CLH 999
 Db 1136 signstyltsksssttyfkrn-----shtdnvsyeh-----sfm-ksgrlrcqfh 1182

RESULT 12
 AAU00207
 ID AAU00207 standard; Protein; 1193 AA.
 XX
 AC AAU00207;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Human novel G-protein coupled receptor, NGPCR#18.

XX
 KW Human; novel G-protein coupled receptor; NGPCR; antagonist;
 KW agonist; diabetes; obesity; atherosclerosis; heart disease;
 KW abnormal blood pressure; cancer.
 OS Homo sapiens.
 XX WO200118207-A1.
 XX 15-MAR-2001.
 PD 08-SEP-2000; 2000WO-US24591.
 XX 10-SEP-1999; 99US-0153366.
 PR 15-NOV-1999; 99US-0165510.
 XX (LEXI-) LEXICON GENETICS INC.
 PA Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;
 PI Sands AT;
 XX WPI; 2001-191773/19.
 DR N-PSDB; AAS00127.
 XX New nucleic acids encoding human G-protein coupled receptors, useful as
 PT a therapeutic target for diabetes, obesity, atherosclerosis, heart
 PT disease and cancer.
 XX Disclosure; Page 109-111; 148pp; English.
 PS The sequence represents a Human novel G-protein coupled receptor (NGPCR).
 XX The NGPCRs are members of the 7 transmembrane domain class of
 CC receptors. The NGPCR proteins of the invention, polynucleotides encoding
 CC them and (ant)agonists of the NGPCRs are useful for the treatment
 CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart
 CC disease, abnormal blood pressure, cancer and any associated symptoms.
 XX Sequence 1193 AA;
 Qy 65 DFDNSSLSPPPAKLVSVFAPSSNEVETTSNDVTLSSLPSNETEKTITIVKTENASG- 123
 Db 278 dstkisvpgngklll-----gsnqneivslkgdiynfrlwnftmakihslnscvkn 332
 Qy 124 -----VKPQRNI-----CNLSSTCNDSAFFRGEIMFOY 151
 Db 333 vvdwqndfwnipnlalkaesnlscgysylipipaaelascadlgticqdgilryisvviq- 391
 Qy 152 DKESTVPQNHITNGTLTGVLSELKRS-----LNKTLQTLSETYFTMCATAEAQSTL 206
 Db 392 -----nllrhpevkqskvaewlnstfgwnyvtvyv-----v 423
 Qy 207 NCTFTIKLNTMNACAAIAALERKIRPMEHCCSVRIPCSPPEELGKL----- 256
 Db 424 nlsfhls-----agedkikvk-----rsledeprlwallvyna 458
 Qy 257 --QCLODQDIVLADHPRGPPFSSQSIPVPRATVLS--QVPKATSAEPDPYSPVTHN 312
 Db 459 tnntnlegkili-----qqkllknesldegrlrhtvnvrglghclameepkgy-----y 507
 Qy 313 VPSPIGEIQP---LSPQPSAPIASSPAIDMPPQSETISSPMPQTHVSGTPPPVKAFSSP 369
 Db 508 wps-----lqpsyvlpcpdkpgfsasri-----cfynatnplv----- 541
 Qy 370 TVSAPANVNT--TSAPPVQTDIVNTS-----SISDLENQVLOMEKALSL-GSLEPNLAG 420
 Db 542 tywgpvdisclickeanevanqilntadgqnltsantivneqvkriynkeeniditlgs 601
 Qy 421 EMINQVSRLLHSPDMLAPLAQRLKLVVDDIGLOLNFSTNT--ISLTSPLALAVIRVNAS 479

Db 602 tlmifsnlssdsdlesssealktidelafkidlnstshvnttrnlalsvssilpg 661
QY 480 SFNTTTFVAQDPAN----LQVSLQETQAPENSIGITITLPSLMMNNLPAHDMELASRVQFNF 535
Db 662 tnaissnfiglpsnnesyfmdfes-gqvdpasvllpnnlenspedsvlrraqftf 720
QY 536 FETPALFODPSLENLSLISYVISSSVANLTVRNLTNRVTVTLKHINPQODELTVRCVFDW 595
Db 721 fntglfdvqgprkrtlsyvmacsignitgnlkdpvqikikhrtdqevhhpi-cafwd 779
QY 596 LGRNGRGWSNDGC-SVKDRRLNETICTCSHLTSGVLDDLSRT-SVLPAQ-MMALTFI 652
Db 780 lnkksfggwntsgcvahrdsdasetvclcnhthfvgvldmldprsaqlarntkvltfi 839
QY 653 TYTGCLSSIFSLVTLTYIAFEKIRRDYPSKILQICAAALLLNVLDDSWIALYKMQ 712
Db 840 syigcgisaisaattlityvafekrrdypskilmlstallfllldgwtstnvd 899
QY 713 GLCISVAVFLHYFLVSTWGLFAHMYLALVKVNTYIRKYILKFCIVGKGVPAVVVT 772
Db 900 glciavavllhfflatftwmgleaahmyialvkvfnvtyrryilkfciigwlpalvvs 959
QY 773 IILTISPDN--YGLGSYGRKFPNGSPDDFCWINNNAVFYTVVGYFCVIFLLNVSMFIVVL 830
Db 960 vllasrnnnevygkesykg---ekgdefcwqdpvfyvtcagyfgvmfllniamfivm 1016
QY 831 VOLCRKIKKQOLGAORQKTSIDERSIAGLTLLGLTGWGFAFGVNNVTFMYLPAFNT 890
Db 1017 vqicgrngkrsnrtdreevlnrlsvsvstfllgwtgafafawgplnlpfmylfsifs 1076
QY 891 LOGFFIFICYVAKENVRKOWRRYLCCGKLKLAENSDSKTATNGLKKTQVNOGVSSSN 950
Db 1077 lqglfifhcamenqgkwrhlcgrfrladnsdsktatnlkssdnlksalss 1136
QY 951 SLOSSS-----NSTNTTLLVNDSCVHAGSNGNASTERNCGVSFVQNGDV--CLH 999
Db 1137 slgnsnlytsksssttyfkrn-----shtdnvsyeh---sin-ksgslrqcfh 1183

RESULT 13
AAU00716
ID AAU00716 standard; Protein; 1193 AA.
AC AAU00716;
XX
AC AAU00716;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human novel G-protein coupled receptor, NGPCR#26.
XX
KW Human; novel G-protein coupled receptor; NGPCR; antagonist;
KW agonist; diabetes; obesity; atherosclerosis; heart disease;
KW abnormal blood pressure; cancer.
XX
OS Homo sapiens.
XX
XX WO200118207-A1.
XX
XX 15-MAR-2001.
XX
XX 08-SEP-2000; 2000WO-US24591.
XX
XX 10-SEP-1999; 99US-01533366.
XX
XX 15-NOV-1999; 99US-0165510.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;
XX Sands AT;
XX WPI; 2001-191773/19.
XX
XX N-PSDB; AAS00135.
XX

PT New nucleic acids encoding human G-protein coupled receptors, useful as
PT a therapeutic target for diabetes, obesity, atherosclerosis, heart
PT disease and cancer -
XX Disclosure; Page 134-136; 149pp; English.
XX
CC The sequence represents a Human novel G-protein coupled receptor (NGPCR).
CC The NGPCRs are members of the 7 transmembrane domain class of
CC receptors. The NGPCR proteins of the invention, polynucleotides encoding
CC them and (ant)agonists of the NGPCRs are useful for the treatment
CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart
CC disease, abnormal blood pressure, cancer and any associated symptoms.
XX
XX Sequence 1193 AA;
QY
Query Match 27.0%; Score 1444.5; DB 22; Length 1193;
Best Local Similarity 34.8%; Pred. No. 5.5e-98;
Matches 354; Conservative 177; Mismatches 293; Indels 193; Gaps 33;
QY 65 DTDNSSLSPPPAKLSVVSFAPSSNEVETTSNDVTLSSLPSNETKTKITIVKTFNASG- 123
Db 278 dstiskvipgngklll-----gsnqneivslkgdiynflwftmnaakilsnscvkn 332
QY 124 -----VKPQRI-----CNLSSICNDSAFFGEIMFQY 151
Db 333 vvdqndfwnipnialkaesnlscgsyilplpaaelascadigtclcgdiyrisvviq- 391
QY 152 DKESTVQNHITNCTLGVLSLSELRSE-----LNKTLQTLSEYFIMCATAEAQSTL 206
Db 392 -----nilrhpekvqskvaewlnstfqwnylyv-----v 423
QY 207 NCTETIKLNTMNACAAIALERKIRMEHCCSVRIPCSPSPPEELGKL----- 256
Db 424 nishls-----agedkikvk-----rsledeprilvallywna 458
QY 257 --QCDLQDPIVCLADHPRGPPSPSSQSPVVPVRAVLVS--QVPKATSFAPPPDYSPVTHN 312
Db 459 tntnlegkii-----qgkllknnesidegrlrlhvtvnrqighclameepky-----y 507
QY 313 VPSPIGEIQP---LSPQPSAPTASSPAIDMPPQSETISSPMPQTHVSGTPPPVKAFFSSP 369
Db 508 wps-----iqpseyvlpckdkpafsari-----cfynatnplv----- 541
QY 370 TVSAPANVNT--TSAPPVQTDIVNTS-----SISLENOVLOMEKALSLSL- 420
Db 542 tywgpvdlsnclkeanevangilnitadqnltsanitniveqkkrivnkeeniditlgs 601
QY 421 EMINQVSRLLHSPDMLAPLAQRLKLVVDIDIGLQNFNTT-LSLTSPSLALAVIRYNAS 479
Db 602 tlmifsnlssdsdlesssealktidelafkidlnstshvnttrnlalsvssilpg 661
QY 480 SFNTTTFVAQDPAN----LQVSLQETQAPENSIGITITLPSLMMNNLPAHDMELASRVQFNF 535
Db 662 tnaissnfiglpsnnesyfmdfes-gqvdpasvllpnnlenspedsvlrraqftf 720
QY 536 FETPALFODPSLENLSLISYVISSSVANLTVRNLTNRVTVTLKHINPQODELTVRCVFDW 595
Db 721 fntglfdvqgprkrtlsyvmacsignitgnlkdpvqikikhrtdqevhhpi-cafwd 779
QY 596 LGRNGRGWSNDGC-SVKDRRLNETICTCSHLTSGVLDDLSRT-SVLPAQ-MMALTFI 652
Db 780 lnkksfggwntsgcvahrdsdasetvclcnhthfvgvldmldprsaqlarntkvltfi 839
QY 653 TYTGCLSSIFSLVTLTYIAFEKIRRDYPSKILQICAAALLLNVLDDSWIALYKMQ 712
Db 840 syigcgisaisaattlityvafekrrdypskilmlstallfllldgwtstnvd 899
QY 713 GLCISVAVFLHYFLVSTWGLFAHMYLALVKVNTYIRKYILKFCIVGKGVPAVVVT 772
Db 900 glciavavllhfflatftwmgleaahmyialvkvfnvtyrryilkfciigwlpalvvs 959
QY 773 IILTISPDN--YGLGSYGRKFPNGSPDDFCWINNNAVFYTVVGYFCVIFLLNVSMFIVVL 830

Db 960 vvlasnnnevygkesygyk---exgdefcwicqdpvfyvtcagfygvmfllniamfivm 1016
 QY 831 VOLCRKKKQOLGAORRTSIODLRSIAGLTLLGLTWGFAFFAWGPNVNTMYLFAIFNT 890
 Db 1017 vqicgrngksnrtlreevlnrlsvslftllgntwgfaffawgplnfpmylfsifns 1076
 QY 891 LQGFIFIFCYCAKENVRKQWRRYLCCGKRLAENSWSKATNGLKKTOTVNGVSSSN 950
 Db 1077 lqglfifhcamkenvgkwrhlccgrfladnsdsktatkniikssdnlgskslss 1136
 QY 951 SLOSSS-----NSTNSTLLVNDSCVHAGNGNASTERNGVSEFVQNGDV--CLH 999
 Db 1137 sigsnstyltsksssttyfkrn-----shdhnvsyeh-----sfn-ksgslrqcfh 1183

RESULT 14
 AAU00210
 ID AAU00210 standard; Protein; 1221 AA.
 XX AAU00210;
 AC 12-SEP-2001 (first entry)
 DT Human novel G-protein coupled receptor, NGPCR#21.
 DE Human; novel G-protein coupled receptor; NGPCR; antagonist;
 KW agonist; diabetes; obesity; atherosclerosis; heart disease;
 KW abnormal blood pressure; cancer.
 XX Homo sapiens.
 OS
 XX WO200118207-A1.
 PN 15-MAR-2001.
 PD 08-SEP-2000; 2000WO-US24591.
 PF 10-SEP-1999; 99US-0153366.
 PR 15-NOV-1999; 99US-0165510.
 XX (LEXI-) LEXICON GENETICS INC.
 PA Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;
 PI Sands AT;
 XX WPI; 2001-191773/19.
 DR N-PSDB; AA500130.
 XX New nucleic acids encoding human G-protein coupled receptors, useful as
 PT a therapeutic target for diabetes, obesity, atherosclerosis, heart
 PT disease and cancer -
 XX Disclosure; Page 118-120; 149pp; English.

XX The sequence represents a Human novel G-protein coupled receptor (NGPCR).
 CC The NGPCRs are members of the 7 transmembrane domain class of
 CC receptors. The NGPCR proteins of the invention, polynucleotides encoding
 CC them and (ant)agonists of the NGPCRs are useful for the treatment
 CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart
 CC disease, abnormal blood pressure, cancer and any associated symptoms.
 XX Sequence 1221 AA;

Query Match 27.0%; Score 1444.5; DB 22; Length 1221;
 Best Local Similarity 34.6%; Pred. No. 5.7e-98;
 Matches 350; Conservative 179; Mismatches 295; Indels 187; Gaps 30;
 QY 65 DTDNSSLSPAPAKLVSVFAPSSNEVETTSNDVTLSSLPSNETEKITIKVTFNASG- 123
 Db 277 dstiskvpgngklll-----gsnqneivslkgdlynlfrlwnftmnaklslnscnvkgn 331

QY 124 -----VKPQRNI-----CNLSSICNDSAFFGEIMFOY 151
 Db 332 vvdqndfnipnlalkaesnlscgsyilipaaealascadgtlclqdggiyrisvviq- 390
 QY 152 DRESTVPQOHITNGTITGVLSLSLSEKRSKSE-----LNKTLQTLSEYFIMCATAEAOSTL 206
 Db 391 -----nllrhpevkvgkvaewlnstfgwnytyvv-----v 422
 QY 207 NCTFTIKLNNMTNACAAIAALERKIRPMEHCSCSRIPCPSPSEELGKL----- 256
 Db 423 nlsfhls-----agedkikvk-----rsledeprlvllwallvyna 457
 QY 257 --OCDLQDPITVCLADHPRGPPFPSSQSIPVPRATVLS--QVPKATSFABPPDPYSPVTHN 312
 Db 458 tntnltlegkii-----qkilkknnesideglrlrlhtvnrqiglhclameepky-----y 506
 QY 313 VPSPIGEIQP---LSQPSAPIASSPAIDMPQSETISSPMPQTHVSGTTPPVKASFSSP 369
 Db 507 wps-----lqpsyvlpcdpkpgfsasri-----cfynatnplv----- 540
 QY 370 TVSAPANVNT--TSAPPVQTDIVNTS-----SISDLENQVLQMEKALS--GSLEPNLAG 420
 Db 541 tywgpvdniscleanevanqilnltadqnltsanitveqkrivnkeeniditlgs 600
 QY 421 EMINQVSRLLHSPDMLAPLAORLLKVVDIGLQLNFSNTT--ISLTSPLSALAVIRNAS 479
 Db 601 tlmifsnllssdsdllesssealktidelfakidlnstshvntnrlalsvslpg 660
 QY 480 SFNTTTFVAODPAN---LQVSLAQAPENSIGTITLPSLNNLPAHDMELASRVQNF 535
 Db 661 tnaifsiglpsnnesyfgmdfes--gvdplaslsvilpnllelspedsvlvrradtf 719
 QY 536 FETPALFQDPSELENLSLTSYVISSVANLTVRNLTRNVTLTKHINPSQDELAVRCVFW 595
 Db 720 fnktgldqvgpqrktlsvymacsignitqnlkdpvqikikhtttgevhpi-cafwd 778
 QY 596 LGRNGRGGSNDGCC--SVKDRRLNETICTCSHLTSEGVLLDLST--SVLPAQ--MMALTFFI 652
 Db 779 lnknsfggwntagcvahrdsdasetvelcnhthfgvldmiprsasqldarntkvtfi 838
 QY 653 TYIGCGLSIFLSVTLVTYIAFEKIRRDYPSKILIQLCALLLNLVFLDLSWTALYKMQ 712
 Db 839 syigcgisaifsaatlityvafekirrdypskilmlstallflnllldgwitsfnvd 898
 QY 713 GLCISAVFLHYFLLVSTWMGLEAFHMYLALVKVFNTRYIRKYILKFCIVGWGVPVYVVT 772
 Db 899 glciavavllhffllatftwmgleaahmyialvkfntyrtlyllkfcilgwpalvvs 958
 QY 773 ILITISPDN--YGLGSYGKFPNGSPDDFCWNNNAVFTYTVGVFCVIFLLNVSMTFVL 830
 Db 959 vvlasnnnevygkesygyk---ekgdefcwicqdpvfyvtcagfygvmfllniamfivm 1015
 QY 831 VOLCRKKKQOLGAORRTSIODLRSIAGLTLLGLTWGFAFFAWGPNVNTMYLFAIFNT 890
 Db 1016 vqicgrngksnrtlreevlnrlsvslftllgntwgfaffawgplnfpmylfsifns 1075
 QY 891 LQGFIFIFCYCAKENVRKQWRRYLCCGKRLAENSWSKATNGLKKTOTVNGVSSSN 950
 Db 1076 lqglfifhcamkenvgkwrhlccgrfladnsdsktatkniikssdnlgskslss 1135
 QY 951 SLOSSS-----NSTNSTLLVNDSCVHAGNGNASTERNGVSEFVQNGDV 995
 Db 1136 sigsnstyltsksssttyfkrn-----shdhsmdksklahadg 1180

RESULT 15
 AAU00206
 ID AAU00206 standard; Protein; 1222 AA.
 XX AAU00206;
 AC 12-SEP-2001 (first entry)
 DT
 XX

QY 567 RNLTRNVTVTLKHINPDSODELTVCVFDWDLGRNGRGWSDNGC-SVKDRRLNETICTCS 625
 Db 71 qnlkdpvqikikhtqtqevhpi-cafdwnknksfgwntsgcvahrdsdasetvclcn 129
 QY 626 HLTSFGVLLDLSRT-SVLPQAQ-MMALFTITYIGCGLSIFLSVTLVYIAFEKIRRDYPS 683
 Db 130 hthfgvldmldprsaqldarntkvtlftisyigcisaifsaatlityvafeklrddyps 189
 QY 684 KILIQCAALLLNVLFLDLSWIALYKMOGLCSVAVFLHYFLVSVFTWGLFAFMYLA 743
 Db 190 kilmlstallflnllldgwitsfnvdlclavavllhffllatftwmgleaahmyia 249
 QY 744 LVKVFNTYIRKYILKFCIVGWGPVAVVVTIILTISPON--YGLGSYGKFPNGSPDDFCWI 801
 Db 250 lvkvfntyirryilkfciigwlpalvsvvlasrnnnevygkesygk---ekgdefcwi 306
 QY 802 NNAVFYITVVGVCVIFLLNVSMFIVLVQLCRITKKKQKOLGAQRKTSIQDLRSIAGLTF 861
 Db 307 qdpvifvvtcagfygvmfflniamfivmvqicgrngkrnsrtlreevlnrlsrsvsltf 366
 QY 862 LLGITWGAFFAWGPVNVTFMYLFAIENTLQGFIFIFCYCAKENVRKQWRYYLCCGKLR 921
 Db 367 llgmtwgfaffawgpnlipfmylfsifnsqglfifhcamkenvqkwrnlccgrfr 426
 QY 922 LAENSDWSKTATNGLKQTVNOGVSSNSLSQSS-----NSTNSTTLLVNNDCSVHAS 975
 Db 427 ladnsdwsktatniikkssdnlglsssssgnstytskskssttyfkrn-----s 480
 QY 976 GNGNASTERNGVSVQNGDV--CLH 999
 Db 481 htdnvsyeh---sfn-ksgslrqcfh 502

RESULT 18
 AAB95487 standard; Protein: 512 AA.
 XX AAB95487;
 AC AAB95487;
 DT 26-JUN-2001 (first entry)
 XX Human protein sequence SEQ ID NO:18020.
 DE Human: primer; detection; diagnosis; antisense therapy; gene therapy.
 KW Homo sapiens.
 OS Homo sapiens.
 PN EP1074617-A2.
 XX EP1074617-A2.
 PD 07-FEB-2001.
 XX 07-FEB-2001.
 PF 28-JUL-2000; 2000EP-0116126.
 XX 28-JUL-2000; 2000EP-0116126.
 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241859.
 XX 09-JUN-2000; 2000JP-0241859.
 PA (HELI-) HELIX RES INST.
 XX Ota T, Isoqai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-318749/34.
 DR
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8; SEQ ID 18020; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAB03166 to AAB13628 and
 CC AAB13633 to AAB18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAB13629 to AAB13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX Sequence 512 AA;
 SQ

Query Match 25.6%; Score 1372.5; DB 22; Length 512;
 Best Local Similarity 52.6%; Pred. No. 3.6e-93;
 Matches 266; Conservative 89; Mismatches 124; Indels 27; Gaps 11;

QY 507 IGTITPSSLMNNLPAHDMELASRVQFFETPALFQDPSLENLSLISYVISSVANLTV 566
 Db 11 lasvilpnllelispedsvlrraqftffnktgldvqgarktlvsvymacsngitl 70
 QY 567 RNLTRNVTVTLKHINPDSODELTVCVFDWDLGRNGRGWSDNGC-SVKDRRLNETICTCS 625
 Db 71 qnlkdpvqikikhtqtqevhpi-cafdwnknksfgwntsgcvahrdsdasetvclcn 129
 QY 626 HLTSFGVLLDLSRT-SVLPQAQ-MMALFTITYIGCGLSIFLSVTLVYIAFEKIRRDYPS 683
 Db 130 hthfgvldmldprsaqldarntkvtlftisyigcisaifsaatlityvafeklrddyps 189
 QY 684 KILIQCAALLLNVLFLDLSWIALYKMOGLCSVAVFLHYFLVSVFTWGLFAFMYLA 743
 Db 190 kilmlstallflnllldgwitsfnvdlclavavllhffllatftwmgleaahmyia 249
 QY 744 LVKVFNTYIRKYILKFCIVGWGPVAVVVTIILTISPON--YGLGSYGKFPNGSPDDFCWI 801
 Db 250 lvkvfntyirryilkfciigwlpalvsvvlasrnnnevygkesygk---ekgdefcwi 306
 QY 802 NNAVFYITVVGVCVIFLLNVSMFIVLVQLCRITKKKQKOLGAQRKTSIQDLRSIAGLTF 861
 Db 307 qdpvifvvtcagfygvmfflniamfivmvqicgrngkrnsrtlreevlnrlsrsvsltf 366
 QY 862 LLGITWGAFFAWGPVNVTFMYLFAIENTLQGFIFIFCYCAKENVRKQWRYYLCCGKLR 921
 Db 367 llgmtwgfaffawgpnlipfmylfsifnsqglfifhcamkenvqkwrnlccgrfr 426
 QY 922 LAENSDWSKTATNGLKQTVNOGVSSNSLSQSS-----NSTNSTTLLVNNDCSVHAS 975
 Db 427 ladnsdwsktatniikkssdnlglsssssgnstytskskssttyfkrn-----s 480
 QY 976 GNGNASTERNGVSVQNGDV--CLH 999
 Db 481 htdnvsyeh---sfn-ksgslrqcfh 502

RESULT 19
 AAU000202 standard; Protein: 541 AA.
 XX AAU000202
 XX AAU000202;
 AC AAU000202;

12-SEP-2001 (first entry)
Human novel G-protein coupled receptor, NGPCR#13.
Human; novel G-protein coupled receptor; NGPCR; antagonist;
agonist; diabetes; obesity; atherosclerosis; heart disease;
abnormal blood pressure; cancer.
Homo sapiens.
WO200118207-A1.
15-MAR-2001.
08-SEP-2000; 2000WO-US24591.
10-SEP-1999; 99US-0153366.
15-NOV-1999; 99US-0165510.
(LEXI-) LEXICON GENETICS INC.
Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;
Sands AT;
WPI; 2001-191773/19.
N-PSDB; AAS00122.
New nucleic acids encoding human G-protein coupled receptors, useful as
a therapeutic target for diabetes, obesity, atherosclerosis, heart
disease and cancer -
Disclosure; Page 99-100; 149pp; English.
The sequence represents a Human novel G-protein coupled receptor (NGPCR).
The NGPCRs are members of the 7 transmembrane domain class of
receptors. The NGPCR proteins of the invention, polynucleotides encoding
them and (ant)agonists of the NGPCRs are useful for the treatment
of diabetes, abnormal body weight or obesity, atherosclerosis, heart
disease, abnormal blood pressure, cancer and any associated symptoms.
Sequence 541 AA;
Query Match 25.6%; Score 1372.5; DB 22; Length 541;
Best Local Similarity 52.4%; Pred. No. 3.9e-93;
Matches 262; Conservative 91; Mismatches 126; Indels 21; Gaps 8;
507 IGTITLPSLLMNLPAHDMELASRVQNFETPALFQDPSLENLSLISVSSVANLTV 566
11 lasvilpnllelspedavlvrraqftffkgtlfgdvgpqrktlvsvymacsigniti 70
567 RNLTRNVTLKHINPSQDELTVRCVFDLGRNGRGWSNCG-SVKDRRLNETICTCS 625
71 qulkdvpqikikhtqtqevhpi-cafdlnknksfgwntsgvahrdsdsatvccln 129
626 HLTSGVLLDLST-SVLPAP-MMALTFIVYICGLSIFLSVLVTVIAEKIRRDYPS 683
130 hfthtgvmdlprisaqldarntkvtffisygicgisaifsaatlityvafeklrddyps 189
684 KILIOCALLLNLLVFLDLSIALYKMOGLCISVAVFLHYFLVFLVFTWMLGFAFMYLA 743
190 kilmlstallfnllldgwitsfnvdglciavavllhffllatftwmlglaahmyia 249
744 LKVENTVIRKILFCIVGWGPAVVVTVIILISPDN--YGLSGSYGFPNGSPDFCWI 801
250 lkvfntvtyrkyllkfcilgwgipalvsvvlarsnmnevgykesygk---ekgdefcwi 306
802 NNAVFTYTVGCVFIFLNVSMETVWLVLQLCRIKKKQLGAKRKTSIQDLRSTAGLTF 861
307 qdpvifvtycaagfygmfflamfivmvgicgrngkrnrtlreevrlrnlsrvsistf 366
862 LLGITWGAFFAWGPVNVTFMYLFAIENTLQGFIFIFYCVAKENVRKQWRYLCCGKLR 921

Db 367 llgmtwgfaffawgplnlpfmylfsifnslgqlffifhcamkenvgkwrhlcgrfr 426
QY 922 LAENDWSKTATNGLKQTVNQGVSSSSNSLOSS-----NSTNSTLLVNDSCSVHAS 975
Db 427 ladnsdsktatnlikksdnlksslsnsgnstyltsksssttyfkrn-----s 480
QY 976 GNGNASTERNQVSPFSQNGD 995
Db 481 htcdasmkdsksklahadgd 500
RESULT 20
AAU00197
ID AAU00197 standard; Protein; 1111 AA.
XX
AC AAU00197;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human novel G-protein coupled receptor, NGPCR#8.
XX
KW Human; novel G-protein coupled receptor; NGPCR; antagonist;
agonist; diabetes; obesity; atherosclerosis; heart disease;
abnormal blood pressure; cancer.
XX
OS Homo sapiens.
XX
PN WO200118207-A1.
XX
PD 15-MAR-2001.
XX
PF 08-SEP-2000; 2000WO-US24591.
XX
PR 10-SEP-1999; 99US-0153366.
PR 15-NOV-1999; 99US-0165510.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;
Sands AT;
XX
DR WPI; 2001-191773/19.
DR N-PSDB; AAS00117.
XX
PT New nucleic acids encoding human G-protein coupled receptors, useful as
a therapeutic target for diabetes, obesity, atherosclerosis, heart
disease and cancer -
XX
PS Disclosure; Page 84-86; 149pp; English.
XX
CC The sequence represents a Human novel G-protein coupled receptor (NGPCR).
CC The NGPCRs are members of the 7 transmembrane domain class of
CC receptors. The NGPCR proteins of the invention, polynucleotides encoding
CC them and (ant)agonists of the NGPCRs are useful for the treatment
CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart
CC disease, abnormal blood pressure, cancer and any associated symptoms.
XX
SQ Sequence 1111 AA;
Query Match 22.5%; Score 1205; DB 22; Length 1111;
Best Local Similarity 33.8%; Pred. No. 2.8e-80;
Matches 310; Conservative 166; Mismatches 306; Indels 136; Gaps 30;
QY 68 NSSLSPPPAKLSVWSPAPSSNE---VETTSINDVTLSPNSETKTKITIVKTFNASCV 124
Db 233 mnl---pvkedidfaefeqiclvwnslsgisgvnfrknyetvpcdstsk-----v 283
QY 125 KPQRNICLSSICNDSAPFRGEIMFYQDKESTVPQNOHITNGTLTGLVLSLSELKSELNK 184
Db 284 ipgngklllgsnqnqlvslkgdl-----ynfrlwnftmnaki-lsnlsncvkn 331

QY	185	TLQTLSETYFMCAATAEAQSTLNC-TFTIKLNN-TMNAACAIAALERVKIRPMEHCCSV	242
Db	332	vvdwqndfwnlpnlalkaesnlscgsylipaaelascadlgtl-----cqatv	381
QY	243	RIPCPSSPEELGKLCQDLQDPVCLADHPR--GPPFSSS---QSIPTVPRATVLSQVPK-	296
Db	382	nspsttpvttnm-----pvtndrkqndgiiyrisvviqnlrhpekvqskvae	435
QY	297	ATSAEPDPDYSPTVTHNV-----PSPIGEIQPLSPQP-----	327
Db	436	lnstfgwnyvtvyvvnifshlsagedkikvksrledeprlvllwallvynatntnlegki	495
QY	328	--SAPIASSPAIDMPPQSETIS-----SPMPQTHVSGTTPPVKASF	366
Db	496	iqqklklnnesldeglrlhtvnrqlghclameepkgyvwpisqseyv--lpcpdkpgf	553
QY	367	S-----SPTVS--APANVNT--TSAPPVQTDIVNTS-----SISDLENOVLQME	406
Db	554	sasricfynatnplvtvgpvdiscnclkeanevanqilnltadggnltsanitniveqvk	613
QY	407	KALSLS-GLSEPNLAGEMINQVSRLLHSPDMLAPLAORLLKVVDIGLQLNFSNNT-LSL	464
Db	614	rivnkeeniiditlgtlmmifsnlssdsdillessealktldelafkidlnstshvni	673
QY	465	TSPSLALAVIRVNASSFNTTFFVAQDPAN----LQVSLQAPENSIGITITLPSLMMNL	520
Db	674	trnlalsvslpgttnaisnfsiglpnnesyfqmdfes-gqvdpilasvilppnllenl	732
QY	521	PAHDELASRVQNFETFPALQDPSLENSLSISYVSSVANLTVRNLTNRVTVTLKHI	580
Db	733	spedsvlrragftfntkgtlqdvqgpktilvsvymacsignititqnlkdpvgkikht	792
QY	581	NPSQDELTVRCVFDLGRNGRGSGSDNCG-SVKORRLNETICTGSHLTSGFVLLDLSRT	639
Db	793	rtqevhhpl-cafdwnknksfgwntsgcvahrdsdasetvclcnhftfhgfvldmldprs	851
QY	640	-SVLPAQ--MMALTFITYICGLSSIFLSVTLVITYIAFEKIRRDYPSKILQOLCAALLLN	697
Db	852	asqldarntkvtifisyigcgisaifsaatlityvafeklrrdyppskilmmstallfn	911
QY	698	LVFLDLSIALYKMOGLCISVAFVFLHYVLLVSTFWGLFAFMVLAIVKVFNTVIRKYL	757
Db	912	lflidgwitsfnvldgclavavllhfflatftwmgleaahmyalvkvfntyirryil	971
QY	758	KFCIVGWGPVAVVWVITILTISPDN--YGLSGYKFPNGSPDDDFCWINNNAVFYITVVGYYF	815
Db	972	kfciiigwlpalvsvvlasrnnnevgyksgyk---ekgdefcwicqdpvifvytcagf	1028
QY	816	CVIFLLNVSMTVWLVLQCRKIKKKQGLQAKRTSIQDLRSIAGLITFLGITWGAFFAWG	875
Db	1029	gvmfflinamfivmvqicgrngkrnsrtlreevlnrlsvvsltflilgntwgfaffawg	1088
QY	876	PVNVTFMVLAIFNTLQOG 893	
Db	1089	pinipfmlfslfnsiqg 1106	
RESULT 21			
ID	AAU00193	standard; Protein; 1112 AA.	
XX	AAU00193;		
AC	AAU00193;		
DT	12-SEP-2001	(first entry)	
XX	Human novel G-protein coupled receptor, NGPCR#4.		
XX	Human; novel G-protein coupled receptor; NGPCR; antagonist;		
KW	agonist; diabetes; obesity; atherosclerosis; heart disease;		
KW	abnormal blood pressure; cancer.		
OS	Homo sapiens.		
XX			

PN	WO200118207-A1.		
XX			
PD	15-MAR-2001.		
XX			
PF	08-SEP-2000; 2000WO-US24591.		
XX			
PR	10-SEP-1999; 99US-0153366.		
PR	15-NOV-1999; 99US-0165510.		
XX	(LEXI-) LEXICON GENETICS INC.		
PA	Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;		
XX	Sands AT;		
PI	WPI; 2001-191773/19.		
DR	N-PSDB; AAS00113.		
XX			
XX	New nucleic acids encoding human G-protein coupled receptors, useful as		
PT	a therapeutic target for diabetes, obesity, atherosclerosis, heart		
PT	disease and cancer -		
XX			
PS	Disclosure; Page 71-73; 149pp; English.		
XX			
CC	The sequence represents a Human novel G-protein coupled receptor (NGPCR).		
CC	The NGPCRs are members of the 7 transmembrane domain class of		
CC	receptors. The NGPCR proteins of the invention, polynucleotides encoding		
CC	them and (ant)agonists of the NGPCRs are useful for the treatment		
CC	of diabetes, abnormal body weight or obesity, atherosclerosis, heart		
CC	disease, abnormal blood pressure, cancer and any associated symptoms.		
XX			
QY	Sequence 1112 AA;		
Query Match 22.5%; Score 1205; DB 22; Length 1112;			
Best Local Similarity 33.8%; Pred. No. 2.8e-80;			
Matches 310; Conservative 166; Mismatches 306; Indels 136; Gaps 30;			
QY	68	NSLSPPPAKLSVVSFAPSNE---VETTSINDVTLSSLPSNETEKITIVKTFNAGSV	124
Db	234	nnal---pykekedifaesfeqiclvwnnsigsvgnfknyetvpcdstisk-----v	284
QY	125	KPORNICNLSSICNDSAFFRGEIMFOYDKRESTVPOQHITNGTLTGLVLSSELKRLNK	184
Db	285	ipngklllgsnqneivslkgdl-----ynrlwnftmnaki-lsnlscnvkgn	332
QY	185	TLQTLSETYFMCAATAEAQSTLNC-TFTIKLNN-TMNAACAIAALERVKIRPMEHCCSV	242
Db	333	vvdwqndfwnlpnlalkaesnlscgsylipaaelascadlgtl-----cqatv	382
QY	243	RIPCPSSPEELGKLCQDLQDPVCLADHPR--GPPFSSS---QSIPTVPRATVLSQVPK-	296
Db	383	nspsttpvttnm-----pvtndrkqndgiiyrisvviqnlrhpekvqskvae	436
QY	297	ATSAEPDPDYSPTVTHNV-----PSPIGEIQPLSPQP-----	327
Db	437	lnstfgwnyvtvyvvnifshlsagedkikvksrledeprlvllwallvynatntnlegki	496
QY	328	--SAPIASSPAIDMPPQSETIS-----SPMPQTHVSGTTPPVKASF	366
Db	497	iqqklklnnesldeglrlhtvnrqlghclameepkgyvwpisqseyv--lpcpdkpgf	554
QY	367	S-----SPTVS--APANVNT--TSAPPVQTDIVNTS-----SISDLENOVLQME	406
Db	555	sasricfynatnplvtvgpvdiscnclkeanevanqilnltadggnltsanitniveqvk	614
QY	407	KALSLS-GLSEPNLAGEMINQVSRLLHSPDMLAPLAORLLKVVDIGLQLNFSNNT-LSL	464
Db	615	rivnkeeniiditlgtlmmifsnlssdsdillessealktldelafkidlnstshvni	674
QY	465	TSPSLALAVIRVNASSFNTTFFVAQDPAN----LQVSLQAPENSIGITITLPSLMMNL	520
Db	675	trnlalsvslpgttnaisnfsiglpnnesyfqmdfes-gqvdpilasvilppnllenl	733

Qy 521 PAHDMELASRVQNFETPALFQDPSPLENLSLISVSISSVANLTVRLNRVTVTLKHI 580
 Db 734 spedsvlvrraqftfnktglfqdvpgqrktlvsvymacsignitqnlkdpvqikht 793
 Qy 581 NPSQDELTVRCVFDLGRNGRGWSNCG-SVKDRRLNETICTCSHLTSFGVLLDLSTR 639
 Db 794 rtqevhhpi-cafwlknksfggwntsgcvahrdsasetvclcnhftghfvgldmldpr 852
 Qy 640 -SVLPAQ-MMALFTIYIGCGLSIFLSVTLVTYIAPEKIRRDYPSKILIOCAALLLN 697
 Db 853 asqldarntkvtlfsyigcisaftltyvafekirrdydpksklmnlstallfn 912
 Qy 698 LVFLDLSWIALYKMOGLCISVAVFLHYFLVLSFTWMGLEAFHMYLALVKVFNTYIRKYL 757
 Db 913 lflldgwitsfnvdlciaavllhffllatftwmgleahmyialkvfntyirryil 972
 Qy 758 KFCIVGWGPVAVVVTIILTISPDN--YGLGSYKFPNGSPDDFCWINNNAVFIYTVGVYF 815
 Db 973 kfciigwglpalvsvvlasrnnnevgykesygk---ekgdefcwldpviyvvtcagf 1029
 Qy 816 CVIFLLNVSMFIVVLQLCRIKKKQLGAQRKTSIQDLRSIAGLTFLLGITWGFAPFAWG 875
 Db 1030 gvmfflniamfivvmvqicgrngkrnsrtlreevlrnlrsvvslflgntwgfafawg 1089
 Qy 876 PNVNFMFLFAFNTLQ 893
 Db 1090 plnlpfmylfsfnslgg 1107

RESULT 22

AAU00201
 ID AAU00201 standard; Protein; 1112 AA.

AC AAU00201;

DT 12-SEP-2001 (first entry)

DE Human novel G-protein coupled receptor, NGPCR#12.

KW Human; novel G-protein coupled receptor; NGPCR; antagonist;
 agonist; diabetes; obesity; atherosclerosis; heart disease;
 abnormal blood pressure; cancer.

OS Homo sapiens.

PN WO200118207-A1.

PD 15-MAR-2001.

PF 08-SEP-2000; 2000WO-US24591.

PR 10-SEP-1999; 99US-0153366.

PR 15-NOV-1999; 99US-0165510.

XX (LEXI-) LEXICON GENETICS INC.

PA Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;
 Sands AT;

DR WPI: 2001-191773/19.

DR N-PSDB; AAS00121.

PT New nucleic acids encoding human G-protein coupled receptors, useful as
 a therapeutic target for diabetes, obesity, atherosclerosis, heart
 disease and cancer -

XX Disclosure; Page 96-99; 149pp; English.

XX The sequence represents a Human novel G-protein coupled receptor (NGPCR).
 CC The NGPCRs are members of the 7 transmembrane domain class of
 CC receptors. The NGPCR proteins of the invention, polynucleotides encoding
 CC them and (antagonists of the NGPCRs are useful for the treatment
 CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart

CC disease, abnormal blood pressure, cancer and any associated symptoms.
 XX
 SQ Sequence 1112 AA;

Query Match 22.5%; Score 1205; DB 22; Length 1112;
 Best Local Similarity 33.8%; Pred. No. 2.8e-80;
 Matches 310; Conservative 166; Mismatches 306; Indels 136; Gaps 30;

Qy 68 NSLSLPPPAKLSSVVSFAPSNE---VETTSINDVTLSSLPSNETEKTKITIVKTFNASGV 124
 Db 234 nual---pvkeedifaesfeqlclvwnnsigsagnvfnrnyetvpcdstisk-----v 284
 Qy 125 KPQRNICNLSSICNDSAFFRGEIMFOYDKESTVPOQHITNGTLGVLSELSELSKLNK 184
 Db 285 ipngngklllgsgnqneivslkgdi-----ynfrlwnftmaki-lsnlscnvkgn 332
 Qy 185 TQIQTSETFIMCATABAQSTLNC-TFTIKLNN-TMCAATAALERVKIRPMHEHCSSV 242
 Db 333 vvdwqndfnipnalakaesnlscgylipaaelascadlgtl-----cqv 382
 Qy 243 RIPCSPSELGKLQCDLQDPIVCLADHPR--GPPFSSS---QSIPVVPVPRATVLSQVPK- 296
 Db 383 nspsttpptvttnm-----pvtndrkqrndgilyrisvignlirhpevkvgkvaew 436
 Qy 297 ATSFAPPPDYSPVTHNV-----PSPIGEIQPLSPQP-----SISDLNQVLOME 327
 Db 437 lnstfgwnytyvynisfhlsagedkikvrsledeprlvllwallvynatnntnlegki 496
 Qy 328 --SAPTASSPAIDMPPQSETIS-----SPMPQTHVSGTTPPVKASF 366
 Db 497 igqklknnesldeglrlhtvnrqlghclameepkgyvwpisqpsyy--lpcdpkpgf 554
 Qy 367 S-----SPTVS--APANVT--TSAPPVQDVIWTS-----SISDLNQVLOME 406
 Db 555 saaricfynatnpltyvgpvdinsclkeanevanqilnltadgqnltsanitniveqvk 614
 Qy 407 KALSL-GSLEPNLAGEMINOVSRLLHSPDMLAPIAQRLLKVVDVDTGLQINFSNTT-ISL 464
 Db 615 rivnkeeniditlgstlmnifsnlssdsdlsesaealktidelafklidnoshvni 674
 Qy 465 TSPSLALAVIRVNASSENTTFVAQDPAN---LQVLETAQAPENSIGITLPSLSMNNL 520
 Db 675 trnlalsvslpgtgnalsnfsiglpnnesyfgmdfes-ggvdpilasvllppnlienl 733
 Qy 521 PAHDMELASRVQNFETPALFQDPSPLENLSLISVSISSVANLTVRLNRVTVTLKHI 580
 Db 734 spedsvlvrraqftfnktglfqdvpgqrktlvsvymacsignitqnlkdpvqikht 793
 Qy 581 NPSQDELTVRCVFDLGRNGRGWSNCG-SVKDRRLNETICTCSHLTSFGVLLDLSTR 639
 Db 794 rtqevhhpi-cafwlknksfggwntsgcvahrdsasetvclcnhftghfvgldmldpr 852
 Qy 640 -SVLPAQ-MMALFTIYIGCGLSIFLSVTLVTYIAPEKIRRDYPSKILIOCAALLLN 697
 Db 853 asqldarntkvtlfsyigcisaftltyvafekirrdydpksklmnlstallfn 912
 Qy 698 LVFLDLSWIALYKMOGLCISVAVFLHYFLVLSFTWMGLEAFHMYLALVKVFNTYIRKYL 757
 Db 913 lflldgwitsfnvdlciaavllhffllatftwmgleahmyialkvfntyirryil 972
 Qy 758 KFCIVGWGPVAVVVTIILTISPDN--YGLGSYKFPNGSPDDFCWINNNAVFIYTVGVYF 815
 Db 973 kfciigwglpalvsvvlasrnnnevgykesygk---ekgdefcwldpviyvvtcagf 1029
 Qy 816 CVIFLLNVSMFIVVLQLCRIKKKQLGAQRKTSIQDLRSIAGLTFLLGITWGFAPFAWG 875
 Db 1030 gvmfflniamfivvmvqicgrngkrnsrtlreevlrnlrsvvslflgntwgfafawg 1089
 Qy 876 PNVNFMFLFAFNTLQ 893
 Db 1090 plnlpfmylfsfnslgg 1107

Db 143 LTNQTLWRTGREGISSTATTILRDVESKYLETALKDPE-----QKVLKIQND----- 190
QY 457 FSNNTISLTSPSLALAVIRVNASSENTTTFAQDPANLOYSL-----ETQAP 503
Db 191 -----SVALETQAITDNCSEERKT-----FNLVQNMNSMDIRCSDIIOGDTQGP 234
QY 504 ENSIGTITLPSLMMNLPALHDMELASRVQNFETPALFQDPSLENLSLIVSSSVAN 563
Db 235 -SAIAFISYSS-----LGNIIATTFE-----EMDKKDQVYLSQVVSAAIGP 276
QY 564 LTVRNLTNRVTVTLKHINPSODELTVRCVFDLGRNGRGG--WSDNGCSCVKDRRLNETIC 622
Db 277 KRNVSLSKSVTLTFQHVKMTPTSKKVCVW---KSTGQGSQMSRDGCFLIHWNKSHTCM 333
QY 623 TCSHLTSFGVLDLSDTSVLPQMMALTFITYICGGLSSIFLSVTLVTVYIAFEKIRRDYP 682
Db 334 NCSSLSSFAVLMALTSQEDP---VLTVTYVGLSVLCLLLAALTFLLCKAIONTST 389
QY 683 SKILIOCAALLLNVLFLDLSWIALYKMQGLCISVAVFLHYFLVSVFTWMLGFAHMYL 742
Db 390 S-LHLQSLCLFLAHLFLVG--IDRTEPKVLCSTIAGALHYLYLAFTWMLLEGVHFL 446
QY 743 AL--VKVFNTRYIRKYLKFCI--VGVGPAVVVTVTLITISPDNYGLSGYKFPNGSPDDF 798
Db 447 TARNLTVVNYSSINRLMKWIMFPGVGVPAVTVASASWPHLYGTA-----DR 495
QY 799 CWINNNAVFTTVGVFCVIFLLNVSMFIVLVOLCRKKKQKOLGAORKTSTODLRSIA- 857
Db 496 CWLHLDQGFMSFELGPVCAIFSANLVFLVFWILKR--KLSSLNSEVST-IQNTMLAF 552
QY 858 ---GLTFLGITWGAFFAWGPVNVVTEMYLEAFNTLOGFFIFIFCYVAKENVRKQWRY 914
Db 553 KATAQLFILGCTWCLGLLOVGPAAQVMAYLFTIINSLOGFFIFLVYCLLSQOVQKQYQKW 612

RESULT 3

US-09-110-116-1
; Sequence 1, Application US/09110116
; Patent No. 6013479
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong
; APPLICANT: Cohan, Victoria L.
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: HUMAN EMRI-LIKE G PROTEIN COUPLED
; FILE REFERENCE: PF-0550 US
; CURRENT APPLICATION NUMBER: US/09/110,116
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 652
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: 429905, EOSINOT03
US-09-110-116-1

Query Match 9.48; Score 500.5; DB 3; Length 652;
Best Local Similarity 29.18; Pred. No. 9.2e-32;
Matches 157; Conservative 92; Mismatches 198; Indels 93; Gaps 19;
QY 398 LENOVL-OMEKALSLGLEPNLAGEMINOVSRLLHSPDPMLAPLQRLKVVDDIGLOLN 456
Db 143 LTNQTLWRTGREGISSTATTILRDVESKYLETALKDPE-----QKVLKIQND----- 190
QY 457 FSNNTISLTSPSLALAVIRVNASSENTTTFAQDPANLOYSL-----ETQAP 503
Db 191 -----SVALETQAITDNCSEERKT-----FNLVQNMNSMDIRCSDIIOGDTQGP 234
QY 504 ENSIGTITLPSLMMNLPALHDMELASRVQNFETPALFQDPSLENLSLIVSSSVAN 563

Db 235 -SVIAFISYSSLGNIIINA-----TFFE-----EMDKKDQVYLSQVVSAAIGP 276
QY 564 LTVRNLTNRVTVTLKHINPSODELTVRCVFDLGRNGRGG--WSDNGCSCVKDRRLNETIC 622
Db 277 KRNVSLSKSVTLTFQHVKMTPTSKKVCVW---KSTGQGSQMSRDGCFLIHWNKSHTCM 333
QY 623 TCSHLTSFGVLDLSDTSVLPQMMALTFITYICGGLSSIFLSVTLVTVYIAFEKIRRDYP 682
Db 334 NCSSLSSFAVLMALTSQEDP---VLTVTYVGLSVLCLLLAALTFLLCKAIONTST 389
QY 683 SKILIOCAALLLNVLFLDLSWIALYKMQGLCISVAVFLHYFLVSVFTWMLGFAHMYL 742
Db 390 S-LHLQSLCLFLAHLFLVG--IDRTEPKVLCSTIAGALHYLYLAFTWMLLEGVHFL 446
QY 743 AL--VKVFNTRYIRKYLKFCI--VGVGPAVVVTVTLITISPDNYGLSGYKFPNGSPDDF 798
Db 447 TARNLTVVNYSSINRLMKWIMFPGVGVPAVTVASASWPHLYGTA-----DR 495
QY 799 CWINNNAVFTTVGVFCVIFLLNVSMFIVLVOLCRKKKQKOLGAORKTSTODLRSIA- 857
Db 496 CWLHLDQGFMSFELGPVCAIFSANLVFLVFWILKR--KLSSLNSEVST-IQNTMLAF 552
QY 858 ---GLTFLGITWGAFFAWGPVNVVTEMYLEAFNTLOGFFIFIFCYVAKENVRKQWRY 914
Db 553 KATAQLFILGCTWCLGLLOVGPAAQVMAYLFTIINSLOGFFIFLVYCLLSQOVQKQYQKW 612

RESULT 4

US-09-110-116-4
; Sequence 4, Application US/09110116
; Patent No. 6013479
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong
; APPLICANT: Cohan, Victoria L.
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: HUMAN EMRI-LIKE G PROTEIN COUPLED
; FILE REFERENCE: PF-0550 US
; CURRENT APPLICATION NUMBER: US/09/110,116
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 344
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: 2935597, GenBank
US-09-110-116-4

Query Match 8.78; Score 463; DB 3; Length 344;
Best Local Similarity 33.5%; Pred. No. 3.4e-29;
Matches 130; Conservative 59; Mismatches 145; Indels 54; Gaps 15;
QY 589 VRCVFDLGRNGRGGWSDNGCSCVKDRRLNETICTCSHLTSFGVLL---DLRSTSVLPQAQ 645
Db 2 VLVCFWEHQGN-CGCHWATTCGTICRTDTSTICRCHLSSFAVLMAYDQEDPV----- 56
QY 646 MMALTFITYICGGLSSIFLSVTLVTVYIAFEKIRRDYPKILIOCAALLLNVLFLDLSW 705
Db 57 ---LTVIYMGVSVLCLLLAALTFLLCKAIONTST--LHLQSLCLFLAHLFLVLAID 112
QY 706 IALYKMQGLCISVAVFLHYFLVSVFTWMLGFAHMYLA---LVKVFNTYIRKYILKFCI- 761
Db 113 QTGHKV--LCSIAGTLHYLYLATFTWMLLEALYLFETARNLTVVNYSSINREMKLMFP 170
QY 762 VGVGPAVVVTVTLITISPDNYGLSGYKFPNGSPDDFCWINNNNAVFTVVGVCVIFLL 821
Db 171 VGVGPAVTVASASRPHLYGTPSR-----CWLQPEKGFITWGLFPGVCAIFS 219
QY 822 NVSMFIVVL-VOLCRICK-KKOLGAORKTSTODLRSIAGTLTFLGITWGAFFAWGPVNV 879

Db 220 NLVFLVLTWILKNRLLSSNSEVSTLRNTRMLAFKATAQL-FILGCTWCLGILQVGPAA 278
QY 880 TFMFLFAFNTLQGFIFIFCYCAKENVRKOWRRYLCCGKRLAENSWSKATNGLKKO 939
Db 279 VMAYLFTIINSLOQVEFLVYCLLSQVREQY-----GK-----WSK-----GIRKL 320
QY 940 TVNQGVSSSSNSLQSSNSNTSTLLVN 967
Db 321 K-----TESEMHTLSSAKADTSKPSTVN 344

RESULT 5
US-09-110-116-3
; Sequence 3, Application US/09110116
; Patent No. 6013479
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong
; APPLICANT: Cohan, Victoria L.
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: HUMAN EMRL-LIKE G PROTEIN COUPLED
; FILE REFERENCE: PF-0550 US
; CURRENT APPLICATION NUMBER: US/09/110,116
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 886
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: 784994, GenBank

US-09-110-116-3

Query Match 8.2%; Score 438; DB 3; Length 886;
Best Local Similarity 20.8%; Pred. No. 1.6e-26;
Matches 198; Conservative 149; Mismatches 365; Indels 238; Gaps 38;

QY 64 EDTNSSLSPPPA-----KLSVVS--FAPSSNE-----VEITSLND-VT 99
Db 79 KDIDECOSPOPCGPNSSCKNLGRYKSCIDGFSPTGNDWVPKPGNFSCDINECLT 138
QY 100 LSLPNSNETKTIIVKTFNAGVYKPNQICNLSSICNDLSAFAFRGEIMFQYDKESTVPO 159
Db 139 SRVCPHS-----DCVNSMGSYSCSCQVGFISRNSTCEDV-----NECADPR 180
QY 160 --NOHIT-NGTL-----TGVLSELKRS-----ELNKTLOTLS 191
Db 181 ACPEHATCNVTGNYSCFPCNPFESSSGHLSQGLKASCEDIDECEMCPINSTCTNTPG 240
QY 192 TYETWCATAEAQSTLNCFTIKLNTMNACAAIAALERVKIRPMEHC-----CCSVRI 246
Db 241 SYFTCHPGFAPSSGQLNFTD-----QVCECRIDECRQDPSTCGPNSIC 285
QY 247 PSSPEELGKQCDLQDPITVCLADHPRGP-----FSSQSI-----PVPVRA 297
Db 286 TNA---LGSYSCG---IVGFHPNPEGSKDGNFSCQVLFKCKEDVDPNKKIQOQCEG 339
QY 298 TSFAEPDPDYPVTHNVPSPGIEQLPSQPSAPIASSPAIDMPPQSETISSPMPQTHVSG 357
Db 340 TA-----
QY 358 TPPPVKASFSPTVSAPANVTTSAPPVQTDIVNTSSISD--LENOVLQMEKALSLSLE 415
Db 342 ---VKPAY-----VSFCAQIN-----NIFSVLDKVCENKTTVVSLKNTTESFV 381
QY 416 PNLAGEMINQVSRLLHSPDMLAPLAQRLLKVVDIGLQNLNFTSNTISLTPSLALAVIR 475
Db 382 P-----VLKQISMWTKFTKEETSSLATVLESVESMTL-ASEFWKPSANVT-PAVRAEYLD 434
QY 476 VNASSFNTTFVAQDPANLOVSLQTPAENSIGTITLPSLMMNLPAHDMELASRVQFNF 535

RESULT 6
US-08-852-806-2
; Sequence 2, Application US/08852806
; Patent No. 5874245
; GENERAL INFORMATION:
; APPLICANT: Shoji Fukusumi
; APPLICANT: Shuji Hinuma
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,806
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,915
; FILING DATE: 16 MAY 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: TAK50002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-852-806-2

Query Match 7.7%; Score 411.5; DB 2; Length 1052;
Best Local Similarity 25.9%; Pred. No. 2.9e-24;
Matches 167; Conservative 99; Mismatches 233; Indels 145; Gaps 29;

```

QY 437 LAPLAQRLLKVVDD-----IGLQNFNTTSLTSPSALAVIR--VNASSEFNTT-----484
DB 187 VSPGSVHLLRVVDEDFHVLGDKAFQSSLIIVD-NLVISIQREPVSASSDITFPMRGR 245
QY 485 -----TFVAQD-----PANLQVLETPQAPENSIGTITLPSLLMNNLPADHM 525
DB 246 RGMKDWVRHSEDRFLFPLKEVLSLSPGKPKATSGAAGSPGRGPGCTVPPG-----PGHSH 300
QY 526 EL---ASRVQNFETFPALFQDPSLENLSLI-----SYVSSSVANLTVRNLTNRN---572
DB 301 QRLLPADPDESSYFVIGAVL---YRTGLGLILPPRPLAVTSRVMTVTVRPTQPPAEP 356
QY 573 -VTVTLKH-INFSQDELTVRCVFDLGR-NGGRGWSNDGSCVKDRRLNETICTCSHLTS 629
DB 357 LITVELSYIINGTTDP---HCASWDYSRADASSGDWDENCOTLETAHAHTRCQOHLST 413
QY 630 FGVL-----LDLSRTSVLPQAMMALFTITYIGCGLSIFLSVTLTYIAFEKIRRDY 681
DB 414 FAVLAQPKDLTLELAGSPSV-----LVIGCAVSCMALLTLAIYAAFWRFIKSE 464
QY 682 FSKILIQCAALLLNVLFLDLSWIALYKMQGLCISAVFLHYFLVFTWMLGLFAFHY 741
DB 465 RSIILLNFCLSLASNILILVGSORVLSK--GVCTMTAAFLHFFELSLFCWVLTAWQSY 522
QY 742 LALVKVFT-YIRKYILKFCIVGWGPVAVVVTITLTIS-PDNYGLGSGKPGSPDDPFC 799
DB 523 LAVIGRMTRLVK---RFLCGLWGLPALVAVSVGTRTKGYGTSSY-----C 568
QY 800 WINNAVFIITVVGFCVIFLLNVSMFIVVLVQLCR-----IKKKOLGAQRKTSIQDL 853
DB 569 WLSLEGLLYAFVGPAAVIVLVNMLIGIIVFNKLMARDGIDSKSKQRAGA-----SL 621
QY 854 RSIAGLTLLGTTWGAFAFW-GPVNVTFMYLFAFNLTLOGFFIFIFYCVAKENVKQWR 912
DB 622 WSSCVVLPALLTMTMSAVLAMTDRRSVLFOALFAVNSAOGFVITAVHCF-----LRREVQ 677
QY 913 RYLCC--GKRLAENSQWKTATNG-----LKKQTVNOGVSSSNSLOSSEN 957
DB 678 DVVKOMGVCRADESDSPDCKNGQLOILSDPEKQVDLACQTV---LFKEVNTCNPSTI 734
QY 958 STNSTLLVNNND-----CSVHASGNGNASTERNGVSPSVQNGDV 996
DB 735 TGTLSRLSLEDEEPKSLVGPBG-----LSFSLPLPGNI 769

```

RESULT 7

US-09-163-669-2
Sequence 2, Application US/09163669
Patent No. 611076
GENERAL INFORMATION:
APPLICANT: FUKUSUMI, SHOJI
APPLICANT: HINUMA, SHOJI
APPLICANT: FUJII, RYO
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED
RECEPTOR (HIBCD07)
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA

COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,669
FILING DATE: 30-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852,806
FILING DATE: 07-MAY-1997
APPLICATION NUMBER: 60/017,915
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: TAK-50002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1052 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-163-669-2

Query Match 7.7%; Score 411.5; DB 3; Length 1052;
Best Local Similarity 25.9%; Pred. No. 2.9e-24;
Matches 167; Conservative 99; Mismatches 233; Indels 145; Gaps 29;

```

QY 437 LAPLAQRLLKVVDD-----IGLQNFNTTSLTSPSALAVIR--VNASSEFNTT-----484
DB 187 VSPGSVHLLRVVDEDFHVLGDKAFQSSLIIVD-NLVISIQREPVSASSDITFPMRGR 245
QY 485 -----TFVAQD-----PANLQVLETPQAPENSIGTITLPSLLMNNLPADHM 525
DB 246 RGMKDWVRHSEDRFLFPLKEVLSLSPGKPKATSGAAGSPGRGPGCTVPPG-----PGHSH 300
QY 526 EL---ASRVQNFETFPALFQDPSLENLSLI-----SYVSSSVANLTVRNLTNRN---572
DB 301 QRLLPADPDESSYFVIGAVL---YRTGLGLILPPRPLAVTSRVMTVTVRPTQPPAEP 356
QY 573 -VTVTLKH-INFSQDELTVRCVFDLGR-NGGRGWSNDGSCVKDRRLNETICTCSHLTS 629
DB 357 LITVELSYIINGTTDP---HCASWDYSRADASSGDWDENCOTLETAHAHTRCQOHLST 413
QY 630 FGVL-----LDLSRTSVLPQAMMALFTITYIGCGLSIFLSVTLTYIAFEKIRRDY 681
DB 414 FAVLAQPKDLTLELAGSPSV-----LVIGCAVSCMALLTLAIYAAFWRFIKSE 464
QY 682 FSKILIQCAALLLNVLFLDLSWIALYKMQGLCISAVFLHYFLVFTWMLGLFAFHY 741
DB 465 RSIILLNFCLSLASNILILVGSORVLSK--GVCTMTAAFLHFFELSLFCWVLTAWQSY 522
QY 742 LALVKVFT-YIRKYILKFCIVGWGPVAVVVTITLTIS-PDNYGLGSGKPGSPDDPFC 799
DB 523 LAVIGRMTRLVK---RFLCGLWGLPALVAVSVGTRTKGYGTSSY-----C 568
QY 800 WINNAVFIITVVGFCVIFLLNVSMFIVVLVQLCR-----IKKKOLGAQRKTSIQDL 853
DB 569 WLSLEGLLYAFVGPAAVIVLVNMLIGIIVFNKLMARDGIDSKSKQRAGA-----SL 621
QY 854 RSIAGLTLLGTTWGAFAFW-GPVNVTFMYLFAFNLTLOGFFIFIFYCVAKENVKQWR 912
DB 622 WSSCVVLPALLTMTMSAVLAMTDRRSVLFOALFAVNSAOGFVITAVHCF-----LRREVQ 677

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QY 913 RYLCC--GKRLAENSWSKTATNG-----LKKQTVNQGVSSSSNSLOSSN 957
 Db 678 DVVKQMGVCRADESESPDCKNGQLQILSDFEKDVLACQTV---LFKEVNTCPNSTI 734
 QY 958 STNSTLLVND-----CSVHASGNGNASTERNNGVSFSVQNGDV 996
 Db 735 TGLSRLSLDEDEPKSLCVGPEG-----LSFSLPLGNI 769

RESULT 8
 US-08-465-976A-2
 ; Sequence 2, Application US/08465976A
 ; Patent No. 5869632
 ; GENERAL INFORMATION:
 ; APPLICANT: SOPPET, DANIEL R
 ; APPLICANT: LI, YI
 ; APPLICANT: ROSEN, CRAIG A
 ; APPLICANT: RUBEN, STEVEN M
 ; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN GILFILLAN, CECCHI
 ; ADDRESSEE: STEWART & OLSTEIN
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NJ
 ; COUNTRY: US
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/465.976A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FERRARO, GREGORY F
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-444
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (201) 994-1700
 ; TELEFAX: (201) 994-1744
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 884 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-465-976A-2

Query Match 6.9%; Score 367.5; DB 2; Length 884;
 Best Local Similarity 25.2%; Pred. No. 7.7e-21;
 Matches 127; Conservative 85; Mismatches 224; Indels 67; Gaps 15;

QY 560 SVANLTVRNLTRNVTVT-----LKHINPSODELTVRCVFDW-LGRNGRGGSNDGC 610
 Db 7 SVAVFHGRNFRGLGILESPISLEFRLLQTANRSK-----AICVQWDPPLGLAQHGVWTARD 62

QY 611 SVKDRRLNETICTSHLTSFGVLLDLSTSVLPQAOMALTFIYICGLSSIFLSVTLVT 670
 Db 63 ELVHRNGSHARCRCSTGTGFLMDASPRERLEGDLLELAVETHVVAVVAVAAVLTA 122

QY 671 YIAEKIRPDYPSKTLIQLCRAALLLNVLFLDSWTALKMGLCISVAVFLHYVLLVSVF 730
 Db 123 LLSRLSKSNVRG--THANVAAALGVAELLFLLG--IHRTHNQLVCTAVALLLHYFFLSTF 179

QY 731 TWMLGELAFMYLALVKVFTYIRKYLKFC--IVGWGVPVAVVTVIILTISPNDYGLGSYK 789
 Db 180 AWFVQGLHLYRMQVEPRN--VDRGAMFEYHALGWGVPVAVLLGLAVGLDPEGY-----230

QY 790 FPNGPSDDFCWNNNAVFIYTVVGYFCVIFLLNVSMFIVVLVOLCRKKKKQLGAORKTS 849
 Db 231 ---GNP-DFCWISVHEPLWISFAGPVVLVIVMNGTFLLAARTSCSTGQRE-----AKTS 282

QY 850 IQDLRSIAGLFLGLITGWGAFFAFMGVNVMTMYLFAIFNTLQGGFFIFIPYCVAKENVRK 909
 Db 283 ALTRSSFFLLLLVSASWLFGLLAVNHSILAFHYLHAGLCGLQGLAVLLFCVLNADARA 342

QY 910 QWRRYLCCGKRLAENS-----DWSKTA---TNGLLKQTVNQGVSSSSNSLSQ--- 954
 Db 343 AWMP-ACLGRKAAPPEARPAPGLGFCAYNNLTALFEESGLIRITLGASTVSVSSARSGR 401

QY 955 -SSNSTNTTLLVNNDCSVHASGNGNAS-----TERNGVSFSVQNGDV 997
 Db 402 QDQSQSGRSYLRDNVLYRHGSAADHTDHSLOAHAGTDLDDVDMFHRDAGADSDSDLS 461

QY 998 LHDFGTGKOHMFNEKEDSCNGKGR 1020
 Db 462 LEEERSLSIPSESEDNGRTRGR 484

RESULT 9
 US-08-982-412-2
 ; Sequence 2, Application US/08982412
 ; Patent No. 5958729
 ; GENERAL INFORMATION:
 ; APPLICANT: SOPPET, DANIEL R
 ; APPLICANT: LI, YI
 ; APPLICANT: ROSEN, CRAIG A
 ; APPLICANT: RUBEN, STEVEN M
 ; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 ; STREET: 9410 KEY WEST AVENUE
 ; CITY: ROCKVILLE,
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/982,412
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROOKES, ANDERS A
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PF181PCT2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8439
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 884 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-982-412-2

Query Match 6.9%; Score 367.5; DB 2; Length 884;
 Best Local Similarity 25.2%; Pred. No. 7.7e-21;
 Matches 127; Conservative 85; Mismatches 224; Indels 67; Gaps 15;

QY 560 SVANLTVRNLTRNVTVT-----LKHINPSODELTVRCVFDW-LGRNGRGGSNDGC 610
 Db 7 SVAVFHGRNFRGLGILESPISLEFRLLQTANRSK-----AICVQWDPPLGLAQHGVWTARD 62

NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 231
TYPE: PRP
ORGANISM: Homosapiens
US-09-370-098-4

Query Match 4.6%; Score 245.5; DB 4; Length 231;
Best Local Similarity 27.5%; Pred. No. 5.9e-12;
Matches 71; Conservative 48; Mismatches 96; Indels 43; Gaps 9;

QY 661 SIF-LSVTLVITYIAFEKIRRDYPSKILQICAAALLNLVFLDLSWIALYKMOG-----L 714
DB 1 SIFCLLLCILTFLVLPQIGS-RTTIHLHCICLFVGSITFL-----AGIENEGQVGLR 54
QY 715 CISVAVFLHYFLVSTWMLGFAHMYLALVKVF--NTYIRKYLKFCIVGVGVPVAVVT 772
DB 55 CRVLVAGLLHYCGLAAGCWSLEGLFLVFLVRFVQGGGLSTRWL---CLIGYGVPLLIWG 111
QY 773 ILTISPDNYGLSGYKGFPGNSPDDFCWANNNAVYITVVCYFVIFLLNVSMFIVLVQ 832
DB 112 VSAIYSKGYGRPY-----CWLDFEQGLWSFLGPTVFIILCNVIFVTTVMK 160
QY 833 LCR-----IKKKQLGAKRKTSIQDLRSIAGLTITWGFAPFAFWGPNVNTFMYL 884
DB 161 LQKFESEINPDMKKLAKARALTITAIQAQ-----FLGCTWVFGLEFIDDRSLVLTIV 213
QY 885 FAIFNTLQGFIFIFVCV 902
DB 214 FTILNCLOGAFLYLLHCL 231

RESULT 13

US-08-811-897A-56
Sequence 56, Application US/08811897A
Patent No. 5858787
GENERAL INFORMATION:
APPLICANT: ONDA, Haruo
APPLICANT: OHTAKI, Tetsuya
APPLICANT: MASUDA, Yasushi
APPLICANT: KITADA, Chieko
APPLICANT: ISHIBASHI, Yoshihiro
APPLICANT: HOSOYA, Masaki
APPLICANT: OGI, Kazuhiro
APPLICANT: MIYAMOTO, Yasunori
APPLICANT: HABATA, Yugo
APPLICANT: SHIMAMOTO, No. 5858787io
TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,897A
FILING DATE: 05-MAR-1997
PRIOR APPLICATION DATA:
CLASSIFICATION: 435
APPLICATION NUMBER: 08/202,986
FILING DATE: February 25, 1994
ATTORNEY/AGENT INFORMATION:

NAME: RESNICK, David S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 44168-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 1324 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-811-897A-56

Query Match 4.5%; Score 240.5; DB 2; Length 1324;
Best Local Similarity 22.9%; Pred. No. 2.5e-10;
Matches 109; Conservative 77; Mismatches 178; Indels 111; Gaps 20;
QY 594 WDLGRNGGRGWS-----NGCSVKDRRLNETICTCSHLTSFGVLLDLSRTSVLP AQM 646
DB 101 YNISRSCTEEGWSQLEPGPYHIACGLND-----RASSLDEQ 137
QY 647 MALTFIY-----IGGLSSIFSLVTLVITYIAFEKIR--RDYPSKILQICAAALLNLV 699
DB 138 QTKFYNTVKTGYTIGYSLSLASLLVAMAILSLFRKLHCTRNYIHMFLW--SPILRATAV 195
QY 700 FLDSLWIALYKMOGL-----CISVAVFLHYFLVSLVSTWMLGFAHMYLALVKVFNT 750
DB 196 FIKD--MALFNSGEIDHCSEASVGCNAVVFQYCVMAFFWLLVEGLYLYTLAVSFFS 253
QY 751 YIRKYLKFCIVGVGVPVAVVTI--ILTISPDNYGLSGYKGFPGNSPDDFCW--INNAV 806
DB 254 E-RKYFWGYLILGWVPSVFTITVTVRIYFEDFG-----CWDTIINSSL 297
QY 807 FYITVVCYFVIFLLNVSMFIVLVQLCRKKKKGAKRKTSIQDLRSIAGLTITLGLIT 866
DB 298 WWI--IKAPILLSILVNFVIFICIIRILYOKLRPPDIG---KNDSSPYSLAKSTLLIPL 353
QY 867 WG--FAFFAWGPNV--TFMYLFAIFNTLQGFIFIFVCV----AKENVKQWRRLCC 917
DB 354 FGIHYVMAFFPDNFKAQVKMVFELVVGSGFQGVVAILYCFELNGEVAQELRRKWRWHLQ 413
QY 918 GKRLAENSWSKATNGLKKQTQVNOGVSSNSNSLOSSNSNSTNTLLVN-----NDCSV 972
DB 414 GVLGWSKSKQHPWGGSGNGATCSTQVSMLTRVSPSARRSS-SFOAEVSLVNHADPFNBCWI 472
QY 973 HASNGNASTERNGVSVSVQNGDVCLHDFGTGKOHMFENEKEDSCNGKRMALRRTS 1027
DB 473 N-----DWSTB-----MPARDNBASEQUENCEDGTNRSAMRPPS 505

RESULT 14

US-08-811-897A-18
Sequence 18, Application US/08811897A
Patent No. 5858787
GENERAL INFORMATION:
APPLICANT: ONDA, Haruo
APPLICANT: OHTAKI, Tetsuya
APPLICANT: MASUDA, Yasushi
APPLICANT: KITADA, Chieko
APPLICANT: ISHIBASHI, Yoshihiro
APPLICANT: HOSOYA, Masaki
APPLICANT: OGI, Kazuhiro
APPLICANT: MIYAMOTO, Yasunori
APPLICANT: HABATA, Yugo
APPLICANT: SHIMAMOTO, No. 5858787io
TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN

Db 278 dstiskvipgngklll-----gsnqneivslkgdiynfrlwnftmnaakilnslscnkvgn 332
 Qy 124 -----VKPQRNI-----CNLSSICNDSAPFRGEIMFOY 151
 Db 333 vvdqndfwnlpnlaikaesnlsccgslplpaaelascadltlcqdgliyrisvviq- 391
 Qy 152 DKESTVPQNHITNGTLTGLVLSLSEKRS-----LNKTLTSETYFIMCATAEAQSTIL 206
 Db 392 -----nilrpevkqsvaewlnstfgwnyvyv-----v 423
 Qy 207 NCTFTIKLNTMNACAAIAALERVKIRPMEHCCSVRIPCSPSPPEELGKL----- 256
 Db 424 nisfnls-----agedkikvk-----rsledeprlvliwallivyna 458
 Qy 257 --QCLOQDPIVCLADHPRGPPFSSSQSIPVVPVPRATVLS--QVPKATSPAEPDPDYSPTVTHN 312
 Db 459 tntnlnlegkii-----qkllknnesideglrlhtvnrqlghclameepkgy-----y 507
 Qy 313 VPSPIGEIQP---LSPQPSAPIASSPAIDMPPQSETISSPMPQTHVSGTPTPPPVKASFSSP 369
 Db 508 wps-----iqpseyvlpcdpkpgfsasri-----cfynatnplv----- 541
 Qy 370 TVSAPANVNT--TSAPPVQDIDVNTS-----SISDLENQVLOMEKALS-OSLEPNLAG 420
 Db 542 tywgpvdisnclkeanevanqilnltadggnlttsanitneiqvkrivnkeeniditlgs 601
 Qy 421 EMINQVSRLLHSPDMLAPLQRLKVVDDIGLOLNFSTT- ISLTSPSLALAVIRVNAS 479
 Db 602 timnifsnlssdsdllessealktidedlafkidlnstshvnttrnlaisvsallpg 661
 Qy 480 SPNTTTFVAQDPAN---LQVLETOQAPENSIGTITLPSLMMNNLPAHDMELASRVQFNF 535
 Db 662 tnaishfsglpsnnesyfgmdfes-gqvdp lasvilppnllenispedsivirraqftf 720
 Qy 536 FETPALFQDPSLENLSLISVSSVANLTVRNLTNRVTTLKHINPSODELTVRCVFD 595
 Db 721 fktgtlfdvgpqrktlsvymacsigitnqkdpvqikkkhtrtqevhhpi-cafwd 779
 Qy 596 LGRNGRGGSNDGC-SVKDRRLNETICTCSHLTSFGVLLDLSRT-SVLPQAQ-MMALTFI 652
 Db 780 lnkksfggwntsgcvahrdsdasetvclcnhftghfvgvldlprsaasqldarntkvtfl 839
 Qy 653 TYIGCGLSIFLSVTLTYTAFEXIRDRDPSKILLIOLCAALLLNLVFLDLSWIALYKMQ 712
 Db 840 syigcisaifsaatlityafeklrdrdpskilmnlstallflnllldgwitsfnvd 899
 Qy 713 GLCISVAVFLHYFLVSVFTWGLEAFHMYLALVKVFNTRYIRKYILKFCIVGCVPAVVVT 772
 Db 900 glciavavllhffllatftwmgleaahmyialkvfntryirylkfcigwglpalvvs 959
 Qy 773 ILTISPDN--YGLGSYGKTPNGSPDDFCWINNNAVFYITVVGVFCVIFLLNVSMFIVVL 830
 Db 960 vvlastnnnevygkesyjk---ekgdefcwiqdpvifvvtcagfygvmfniamfivvm 1016
 Qy 831 VOLCRITKXKQLGAQRKTSIQLDRSIAGLTLLGTTWGFAPFAGVFNVTMYLFAIFNT 890
 Db 1017 vqicgrngkrnsrntlreevlnrlsvslftilgmntwgtfaffawgplnlpfmylfsifs 1076
 Qy 891 LOG 893
 Db 1077 lqg 1079

Search completed: May 23, 2002, 07:37:55
 Job time: 160 sec

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; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,897A
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: February 25, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-811-897A-18

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Query Match 4.4%; Score 233; DB 2; Length 448;
Best Local Similarity 23.2%; Pred. No. 1.7e-10;
Matches 92; Conservative 75; Mismatches 145; Indels 84; Gaps 19;

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QY 596 LGRNGRGWSD-----NGCSVKDRRLNETICTCSHLTSGVLLDLSRTSVLPQMMAL 649
Db 94 VGRNCTEDGWSEPPHYFDACGDDYE-----PESGDQDYIYLSV 133
QY 650 TFIYVIGCGLSIFLSVTLVTYIAFEKIR--RDYPSKILIOALCAALLLNLFVLLDSWTA 707
Db 134 KALYTVGVSTSLATLTAMVILCRFKLHCTRNF---IHMNLFVSMFLRAISVFKDWT- 189
QY 708 LYKMOGL-----CISVAVFLHYFLVSTWMLGAEAFHMYLALVKVFNITYIRKYILK 758
Db 190 LYAEDSSHCFSVSTVECKAVMVFHYCVVSNYFWLFTGLYLFETLLVETFFPE--RRYFW 248
QY 759 FCIVGWGVPVAVVTI--ILTIISPDNYGLSGYKFPNGSPDDFCWINNN--AVFYI---TV 811
Db 249 YTIIGWGTPVTCVTMAVRLYFDDAG-----CWDMDNDSTALMWWYIKGPV 293
QY 812 VGYFCVIFLLNVSMFIVLVOLCRIRKKKOLGAQRKTSIODLSRIAGLTFLLGITWGEAF 871
Db 294 VGSIMNVNVLFIGI--IIILVQ--KLOSPDMGNGESSIYLRARSTLLIPLFGI--HTV 348
QY 872 FAWGPVNVVT--FMYLFAI--FNTLQGFIFIFYCV-----AKENVRKQWRRYLCCGKRLAE 924
Db 349 FAFSPENYSKRERLVFELGLSGFQGVVAVLYCFNGEVOAEIKRWRSW----KVNRYF 404
QY 925 NSDWS-----KATNGLKKQTVNQGVSSSSNSLQSSS 956
Db 405 TMDFKHRHPSLASSGVNGTQLSILSKSSQLRMSS 440

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RESULT 15
US-08-855-213-18
; Sequence 18, Application US/08855213
; Patent No. 5892004
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya

```

```

; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 589200410
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR
; PREPARING SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,213
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: 25-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-855-213-18

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Query Match 4.4%; Score 233; DB 2; Length 448;
Best Local Similarity 23.2%; Pred. No. 1.7e-10;
Matches 92; Conservative 75; Mismatches 145; Indels 84; Gaps 19;

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```

QY 596 LGRNGRGWSD-----NGCSVKDRRLNETICTCSHLTSGVLLDLSRTSVLPQMMAL 649
Db 94 VGRNCTEDGWSEPPHYFDACGDDYE-----PESGDQDYIYLSV 133
QY 650 TFIYVIGCGLSIFLSVTLVTYIAFEKIR--RDYPSKILIOALCAALLLNLFVLLDSWTA 707
Db 134 KALYTVGVSTSLATLTAMVILCRFKLHCTRNF---IHMNLFVSMFLRAISVFKDWT- 189
QY 708 LYKMOGL-----CISVAVFLHYFLVSTWMLGAEAFHMYLALVKVFNITYIRKYILK 758
Db 190 LYAEDSSHCFSVSTVECKAVMVFHYCVVSNYFWLFTGLYLFETLLVETFFPE--RRYFW 248
QY 759 FCIVGWGVPVAVVTI--ILTIISPDNYGLSGYKFPNGSPDDFCWINNN--AVFYI---TV 811
Db 249 YTIIGWGTPVTCVTMAVRLYFDDAG-----CWDMDNDSTALMWWYIKGPV 293
QY 812 VGYFCVIFLLNVSMFIVLVOLCRIRKKKOLGAQRKTSIODLSRIAGLTFLLGITWGEAF 871
Db 294 VGSIMNVNVLFIGI--IIILVQ--KLOSPDMGNGESSIYLRARSTLLIPLFGI--HTV 348
QY 872 FAWGPVNVVT--FMYLFAI--FNTLQGFIFIFYCV-----AKENVRKQWRRYLCCGKRLAE 924

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Db 349 FAFSPENSVKRRRLVFLGLGSGFGVAVLYCFLNGEVAQAEIKKRWSW-----KVNRYF 404
 QY 925 NSDWS-----KTAATGLKKQTVNQGVSSSSNSLQSSS 956
 Db 405 TMDFKHRHPSLASSGVNGGTQLSLSKSSSSLRMSS 440

RESULT 16

US-08-811-897A-19
 ; Sequence 19, Application US/08811897A
 ; Patent No. 5858787
 ; GENERAL INFORMATION:
 ; APPLICANT: ONDA, Haruo
 ; APPLICANT: OHTAKI, Tetsuya
 ; APPLICANT: MASUDA, Yasushi
 ; APPLICANT: KITADA, Chieko
 ; APPLICANT: ISHIBASHI, Yoshihiro
 ; APPLICANT: HOSOYA, Masaki
 ; APPLICANT: OGI, Kazuhiro
 ; APPLICANT: MIYAMOTO, Yasunori
 ; APPLICANT: HABATA, Yugo
 ; APPLICANT: SHIMAMOTO, No. 5858787io
 ; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING
 ; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 ; ADDRESSEE: CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: US
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/811.897A
 ; FILING DATE: 05-MAR-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/202,986
 ; FILING DATE: February 25, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RESNICK, David S.
 ; REGISTRATION NUMBER: 34235
 ; REFERENCE/DOCKET NUMBER: 44168-DIV
 ; TELEPHONE: (617)523-3400
 ; TELEFAX: (617)523-6440
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 467 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-811-897A-19

Query Match 4.4%; Score 233; DB 2; Length 467;
 Best Local Similarity 23.2%; Pred. No. 1.9e-10;
 Matches 92; Conservative 75; Mismatches 145; Indels 84; Gaps 19;

QY 596 LGRNGRGGSWD-----NGCSVKDRRLNETTCTCSHLTSFGVLLDLRTSVLPQAQMAL 649
 Db 113 VGRNCTEDGSEPFPHYDFACGFDYE-----PESGDQDYIYLSV 152
 QY 650 TFIYVIGGLSISFLVTVVIAEKIR--RDYPSKILQLCAALLLNVLFLDLSWIA 707
 Db 153 KALYTVGYSTSLATLTAMVILCRFKLCTRF---IHMNLFVSPMLRAISVFIKDWI- 208

QY 708 LYKMOGL-----CISVAVFLHYFLVSVFTWGLEAFHMYLALVKVENTYIRKYLK 758
 Db 209 LYAODSSHCFSVTECKAVAVFFHYCVSVNYFWLFIELGLYFLTLVETFPPE-RRVEYF 267
 QY 759 FCIYVGWGPVAVVTI--ILTISPDNYGLSGYKGFNGSPDPCFWINN--AVFYI---TV 811
 Db 268 YTIIGWGTPVTCVTWAVLRYFDAG-----CWMNDSTALWVVIKGPV 312
 QY 812 VGYFCVIFLLNVSMEIVLVQLCRKKKQLGAQRKTSIQDLRSIAGLTPLLGITWGF 871
 Db 313 VGSIMVNFVFIGI-ILILVQ--KLQSPDMGNNESSIYLRKARSTLLPLPLFGI--HYTV 367
 QY 872 FAWGPVNVIT--FMYLFAI-FNTLQGFIFIFYCV-----AKENVRKQWRRYLCCKGLRLAE 924
 Db 368 FAFSPENSVKRRRLVFLGLGSGFGVAVLYCFLNGEVAQAEIKKRWSW-----KVNRYF 423
 QY 925 NSDWS-----KTAATGLKKQTVNQGVSSSSNSLQSSS 956
 Db 424 TMDFKHRHPSLASSGVNGGTQLSLSKSSSSLRMSS 459

RESULT 17

US-08-855-213-19
 ; Sequence 19, Application US/08855213
 ; Patent No. 5892004
 ; GENERAL INFORMATION:
 ; APPLICANT: ONDA, Haruo
 ; APPLICANT: OHTAKI, Tetsuya
 ; APPLICANT: MASUDA, Yasushi
 ; APPLICANT: KITADA, Chieko
 ; APPLICANT: ISHIBASHI, Yoshihiro
 ; APPLICANT: HOSOYA, Masaki
 ; APPLICANT: OGI, Kazuhiro
 ; APPLICANT: MIYAMOTO, Yasunori
 ; APPLICANT: HABATA, Yugo
 ; APPLICANT: SHIMAMOTO, No. 5892004io
 ; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR
 ; TITLE OF INVENTION: PREPARING SAID PROTEIN, AND USE THEREOF
 ; NUMBER OF SEQUENCES: 55
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 ; ADDRESSEE: CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: US
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/855,213
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/202,986
 ; FILING DATE: 25-FEB-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RESNICK, David S.
 ; REGISTRATION NUMBER: 34235
 ; REFERENCE/DOCKET NUMBER: 44168
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)523-3400
 ; TELEFAX: (617)523-6440
 ; TELEX: 200291 STRE UR
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 467 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-855-213-19
Query Match 4.4%; Score 233; DB 2; Length 467;
Best Local Similarity 23.2%; Pred. No. 1.9e-10;
Matches 92; Conservative 75; Mismatches 145; Indels 84; Gaps 19;

QY 596 LGRNGRGWSD-----NGCSVKDRRLNETICTSHLTSGVGLDLSRTSVLPQMMAL 649
Db 113 VGRNCTEDGSEPPHYFDACGDDYE-----PESGDQDYYIYLSV 152
QY 650 TFIYIGGLSIFSVTLVTYIAFKIR--RDYPSKILQLCAALLNLNLFVLDWSIA 707
Db 153 KALYTVGYSTSLATLTAMVILCRFKLHCTRF---IHMNLVSEFMLRAISVFIKDWI- 208
QY 708 LYKMQGL-----CISVAVFLHVLVSVFTWGLEAFHMLALVKVFTYIRKYILK 758
Db 209 LYAEQDSHCFVSTVECKAVMFFHYCVVSNFYFLFIEGLYFTLLVETFPPE-RRYFYW 267
QY 759 FCIVGWGVPVAVVTI--ILTISPNDYGLSGYKFPNGSPDDFCWNNNN--AVEYI---TV 811
Db 268 YTIIGWGTPVCTVWVRLVYDDAG-----CWDMDSTALWVWIKGPV 312
QY 812 VGYFCVIFLLNVSMFIVVLQCRKKKQKOLGAQRKTSIODLRSIAGLTFLLGITWGF 871
Db 313 VGTWNVNVLFIGI-IIIIVQ--KLQSPDMGNGNESSIYLRARSTLLIPLFGI--HYTV 367
QY 872 FAWGPVNVV--FMVLFAT-FNTLOGFFIFICYV---AKENVRKORRYLCCGKRLAE 924
Db 368 FAFSPENVSKRERLVFELGLSGFQGVVAVLCFLNGEVOAEIKRWSW---KVNRYF 423
QY 925 NSDWS----KTATNGLKKQTVNQGVSSSSNSLQSS 956
Db 424 TMDPKRHRPSLASSGVNGTQLSILSKSSQLRMSS 459

RESULT 18

US-08-811-897A-16
; Sequence 16, Application US/08811897A
; Patent No. 5858787
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 5858787io
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811.897A
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

RESULT 19

US-08-855-213-16
; Sequence 16, Application US/08855213
; Patent No. 5892004
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 5892004io
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR
; TITLE OF INVENTION: PREPARING SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 55

APPLICATION NUMBER: 08/202,986
FILING DATE: February 25, 1994
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, David S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 44168-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-811-897A-16
Query Match 4.3%; Score 231.5; DB 2; Length 448;
Best Local Similarity 21.8%; Pred. No. 2.3e-10;
Matches 103; Conservative 88; Mismatches 165; Indels 117; Gaps 23;

QY 521 PAH--DMELASRVQ-FNFETPALFQDPSLENLSLISYVSSSVANLTVRNLRTVTL 577
Db 46 PAHVGMVLVSCPELFRIFNPQVWE---TETIGFQFADSKSLDLSMDRVVSRNCT--- 99
QY 578 KHINPSODELTVRCVFDLGRNGRGWSD-----NGCSVKDRRLNETICTSHLTSG 631
Db 100 -----EDGWSEPPHYFDACGFEYE----- 120
QY 632 VLDSLRTSVLPQMMALTFITYIGGLSIFLSVLTVYIAFEKIR--RDYPSKILQL 689
Db 121 ----SETGDQDYYVLSVKALYTVGYSTSLVTLTAMVILCRFKLHCTRF---IHMNL 172
QY 690 CAALLLNLFVLDWSIALYKMQGL-----CISVAVFLHVLVSVFTWMLEAFHM 740
Db 173 FVSPMLRAISVFIKDWI-LYAEQDSNHCFVSTVECKAVMFFHYCVVSNFYFLFIEGL 231
QY 741 YLALVKVFTYIRKYILKFCIVGWGVPVAVVTI--ILTISPNDYGLSGYKFPNGSPDF 798
Db 232 FTLVETFPPE-RRYFYWIIIGWGTPTVCVSWMLRLYFDDTG----- 275
QY 799 CW--INNNAVEYI---TVVGYFCVIFLLNVSMFIVVLQCRKKKQKOLGAQRKTSIODL 853
Db 276 CWDMDNTALWVWIKGPVVGSIWNVFLFIGI-IVILVQ--KLQSPDMGNGNESSIYLR 332
QY 854 RSIAGLTFLLGITWGFQFAFANGCPVNVV--FMVLFAT-FNTLOGFFIFICYV---AKEN 906
Db 333 RSTLLIPLFGI--HYTVFAFSPENVSKRERLVFELGLSGFQGVVAVLCFLNGEVOAE 390
QY 907 VRKOWRRLCCGKRLRAENSOWS----KTATNGLKKQTVNQGVSSSSNSLQSS 955
Db 391 IKRWRSW---KVNRYFTMDFKRHRPSLASSGVNGTQLSILSKSSQIRMS 439

Db 210 FVSMRLRAISVFIKDWI-LXAEQDSNHCFSVSTVECKAVMVFHYCVSNVFWLFIKGLYL 268
 QY 741 YLALVKVNTYIRKYLKFCIVGWPVAVVTI--ILTSPDNYGLSGYKFPNGSPDDF 798
 Db 269 FTLLVETFEPE--RRYFYWYIIIGWGTTCVCSVWMLRLYFDDTG----- 312
 QY 799 CW--INNNAVYI---TVVGYFCVIFLLNVSMFIVLVOLCRKIKKKQKQAKRKTISIQDL 853
 Db 313 CWDMDNTALMWIKPVGVSIMVNFVFIGI-IVILVQ--KLQSPDMGNGESSIYLRLA 369
 QY 854 RSIAGTLFLGITWGAFFAWGPVNVIT--FMYLFAI-FNTLQGFIFIFYCV-----AKEN 906
 Db 370 RTLLLIPLFGI--HYTVFAFSPENVSKRRLVFLGSGFQGVVAVLYCFLNGEVQAE 427
 QY 907 VRKQWRYLCCGKRLAENSQWS-----KTATNGLKKQTVNOGVSSSSSSSQSS 955
 Db 428 IRRKRSW---KVNRYFTMDFKRRHPSLASSGVNGGTQLSILSKSSQIRMS 476

RESULT 21

US-08-855-213-17
 ; Sequence 17, Application US/08855213
 ; Patent No. 5892004
 ; GENERAL INFORMATION:
 ; APPLICANT: ONDA, Haruo
 ; APPLICANT: OHTAKI, Tetsuya
 ; APPLICANT: MASUDA, Yasushi
 ; APPLICANT: KITADA, Chieko
 ; APPLICANT: ISHIBASHI, Yoshihiro
 ; APPLICANT: HOSoya, Masaki
 ; APPLICANT: OGI, Kazuhiro
 ; APPLICANT: MIYAMOTO, Yasunori
 ; APPLICANT: HABATA, Yugo
 ; APPLICANT: SHIMAMOTO, No. 58920041o
 ; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR
 ; PREPARING SAID PROTEIN, AND USE THEREOF
 ; NUMBER OF SEQUENCES: 55
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 ; ADDRESSEE: CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: US
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/855,213
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/202,986
 ; FILING DATE: 25-FEB-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RESNICK, David S.
 ; REGISTRATION NUMBER: 34235
 ; REFERENCE/DOCKET NUMBER: 44168
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)523-3400
 ; TELEFAX: (617)523-6440
 ; TELEX: 200291 STRE UR
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 485 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-855-213-17

Query Match 4.3%; Score 231.5; DB 2; Length 485;
 Best Local Similarity 21.8%; Pred. No. 2.6e-10;
 Matches 103; Conservative 88; Mismatches 165; Indels 117; Gaps 23;
 QY 521 PAH--DMELASRYO-FNEFFETPALFOFDSLENLSLVSVISSVANLTVRNLTRNVTVL 577
 Db 83 PAHGVEMLVSCPELFRIFNPQVWE---TETIGFEGADSKSLDSMDRVSRNCT--- 136
 QY 578 KHINPSQDELTVRCVFDLGRNGRGGWS-----NGCSVKDRRLNETICTCSHLTSFG 631
 Db 137 -----EDGWSPEFPHYFDACGPEYE----- 157
 QY 632 VLILDSRTSVLPQMMALTFITYIGCGLSIFSLVTLTYTAFKIR--RDYPSKILIQ 689
 Db 158 -----SETGDQDYYSVSKALYTVGYSTSLVTLTAMVILCRKHLCTRNF---IHMNL 209
 QY 690 CAALLLNLFVLDLSWIALYKMOGL-----CISVAVFLHYFLVFTWMLGFAFM 740
 Db 210 FVSEMLRAISVFIKDWI-LXAEQDSNHCFSVSTVECKAVMVFHYCVSNVFWLFIKGLYL 268
 QY 741 YLALVKVNTYIRKYLKFCIVGWPVAVVTI--ILTSPDNYGLSGYKFPNGSPDDF 798
 Db 269 FTLLVETFEPE--RRYFYWYIIIGWGTTCVCSVWMLRLYFDDTG----- 312
 QY 799 CW--INNNAVYI---TVVGYFCVIFLLNVSMFIVLVOLCRKIKKKQKQAKRKTISIQDL 853
 Db 313 CWDMDNTALMWIKPVGVSIMVNFVFIGI-IVILVQ--KLQSPDMGNGESSIYLRLA 369
 QY 854 RSIAGTLFLGITWGAFFAWGPVNVIT--FMYLFAI-FNTLQGFIFIFYCV-----AKEN 906
 Db 370 RTLLLIPLFGI--HYTVFAFSPENVSKRRLVFLGSGFQGVVAVLYCFLNGEVQAE 427
 QY 907 VRKQWRYLCCGKRLAENSQWS-----KTATNGLKKQTVNOGVSSSSSSSQSS 955
 Db 428 IRRKRSW---KVNRYFTMDFKRRHPSLASSGVNGGTQLSILSKSSQIRMS 476

RESULT 22

US-08-811-897A-20
 ; Sequence 20, Application US/08811897A
 ; Patent No. 5858787
 ; GENERAL INFORMATION:
 ; APPLICANT: ONDA, Haruo
 ; APPLICANT: OHTAKI, Tetsuya
 ; APPLICANT: MASUDA, Yasushi
 ; APPLICANT: KITADA, Chieko
 ; APPLICANT: ISHIBASHI, Yoshihiro
 ; APPLICANT: HOSoya, Masaki
 ; APPLICANT: OGI, Kazuhiro
 ; APPLICANT: MIYAMOTO, Yasunori
 ; APPLICANT: HABATA, Yugo
 ; APPLICANT: SHIMAMOTO, No. 58587871o
 ; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
 ; SAID PROTEIN, AND USE THEREOF
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 ; ADDRESSEE: CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: US
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/811,897A
 ; FILING DATE: 05-MAR-1997
 ; CLASSIFICATION: 435

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: February 25, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-811-897A-20

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Query Match      4.3%; Score 231; DB 2; Length 476;
Best Local Similarity 22.6%; Pred. No. 2.8e-10;
Matches 95; Conservative 74; Mismatches 146; Indels 106; Gaps 20;

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QY 596 LGRNGRGWSD-----NGSVKDRRLNETICTSHLTSGVLLDLSTSVLPQAQMMAL 649
DB 94 VGRNCTEDGSEPPHYFDACGDDYE-----PESGDQDYVYLSV 133
QY 650 TFIYIGGLSSIFLSVTLVYIAFEKIR--RDYPSKILQICALLLLNLVFLDLSWIA 707
DB 134 KALYTVGYSTSLATLTAMVILCRFRKLHCTRN-----IHMNLFSFMLRAISVFIKDWI- 189
QY 708 LYKMOGL-----CISVAVFLHYFLVSTWGMGLEAFHMYLALVKVNTYIRKYILK 758
DB 190 LYAQDSSHCHFSVTECKAVMVFHYCVVSNFYFLFIEGLYFTLLVETFPPE-RRYFYW 248
QY 759 FCIVGWGVPVAVVTI--ILTISPNDYGLSGYKFPNGSPDDFCWINNN--AVFYI---TV 811
DB 249 YTIIGWGTPTCVTVWVAVLRYFDAG-----CWMNDSTALWVVIKGPV 293
QY 812 VGYFCVFLNVSMTVL-----VOLCRIRKKKQKLAQKRTSIQD 852
DB 294 VGSIMVNFVIGIILVQKQSPDMGNGNESSIYFSCVQKCYC--KPQRAQOHSCKMSE 351
QY 853 LRSI-----AGLTFLLGITWG--FAFFANGPVNVT--FMYLFAI-FNTLQGFIFIFYCV- 902
DB 352 LSTITRLARSTLLPLFGIHYTVFAFSPENVSKRERLVFELGLSGFQGVVAVLYCFL 411
QY 903 ---AKENVKQWRRYLCCGKRLAENSOWS----KTATNGLKQTVNGVSSSSNSLOSS 955
DB 412 NGEVOAEIKRWRSW----KVNRYFTMDFKHRHPSLASSGVNGGTQLSILSKSSQLRMS 467
QY 956 S 956
DB 468 S 468

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```

RESULT 23
US-08-855-213-20
; Sequence 20, Application US/08855213
; Patent No. 5892004
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 589200410
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR
; PREPARING SAID PROTEIN, AND USE THEREOF

```

```

; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ATTORNEY/AGENT INFORMATION:
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,213
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: 25-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-855-213-20

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Query Match      4.3%; Score 231; DB 2; Length 476;
Best Local Similarity 22.6%; Pred. No. 2.8e-10;
Matches 95; Conservative 74; Mismatches 146; Indels 106; Gaps 20;

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```

QY 596 LGRNGRGWSD-----NGSVKDRRLNETICTSHLTSGVLLDLSTSVLPQAQMMAL 649
DB 94 VGRNCTEDGSEPPHYFDACGDDYE-----PESGDQDYVYLSV 133
QY 650 TFIYIGGLSSIFLSVTLVYIAFEKIR--RDYPSKILQICALLLLNLVFLDLSWIA 707
DB 134 KALYTVGYSTSLATLTAMVILCRFRKLHCTRN-----IHMNLFSFMLRAISVFIKDWI- 189
QY 708 LYKMOGL-----CISVAVFLHYFLVSTWGMGLEAFHMYLALVKVNTYIRKYILK 758
DB 190 LYAQDSSHCHFSVTECKAVMVFHYCVVSNFYFLFIEGLYFTLLVETFPPE-RRYFYW 248
QY 759 FCIVGWGVPVAVVTI--ILTISPNDYGLSGYKFPNGSPDDFCWINNN--AVFYI---TV 811
DB 249 YTIIGWGTPTCVTVWVAVLRYFDAG-----CWMNDSTALWVVIKGPV 293
QY 812 VGYFCVFLNVSMTVL-----VOLCRIRKKKQKLAQKRTSIQD 852
DB 294 VGSIMVNFVIGIILVQKQSPDMGNGNESSIYFSCVQKCYC--KPQRAQOHSCKMSE 351
QY 853 LRSI-----AGLTFLLGITWG--FAFFANGPVNVT--FMYLFAI-FNTLQGFIFIFYCV- 902
DB 352 LSTITRLARSTLLPLFGIHYTVFAFSPENVSKRERLVFELGLSGFQGVVAVLYCFL 411
QY 903 ---AKENVKQWRRYLCCGKRLAENSOWS----KTATNGLKQTVNGVSSSSNSLOSS 955
DB 412 NGEVOAEIKRWRSW----KVNRYFTMDFKHRHPSLASSGVNGGTQLSILSKSSQLRMS 467
QY 956 S 956
DB 468 S 468

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RESULT 24

US-08-811-897A-21
; Sequence 21, Application US/08811897A
; Patent No. 5858787
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 5858787io
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,897A
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: February 25, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 495 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-811-897A-21

Query Match 4.3%; Score 231; DB 2; Length 495;
Best Local Similarity 22.6%; Pred. No. 3e-10;
Matches 95; Conservative 74; Mismatches 146; Indels 106; Gaps 20;

QY 596 LGRNGRGWSD-----NGCSVKDRRLNETICTCSHLTSGVLLDLSTSVLPQMMAL 649
Db 113 VGRNCTGDWSEFPFHYFDACGDDYE-----PESGDQDYIYLSV 152

QY 650 TPITYIGCLSLISFLSVLTIVYIAFEKIR--RDYPSKILQICAAALLNLNLFLLDSWTA 707
Db 153 KALYTVGYSTSLATLTAMVILCRFKLHTRNP---IHMNLFVSFMLRAISVFIDWIL- 208
QY 708 LYKMOGL-----CISVAVFLHYFLVSVFTWGLFAFHMVLAIVKVFNTYIRKIYILK 758
Db 209 LYAEQDSSHCFSVTECKAVMVFHYCVSVSNFYFLFIEGLVFLTLVETFPPE-RRYFYW 267
QY 759 FCIVGWGVPVAVVTI---ILTISPDNIGLGSYGKFPNGSPDDFCWINNN--AVFYI---TV 811

Db 268 YTIIGWGTPTVCVTVMVAVRLYFDAG-----CWMNDSTALWVVKGPV 312
QY 812 VGFCVIFELLNVSMEFVVL-----VOLCRIKKKKOLGAQRKTSIQD 852
Db 313 VGSIMVNFVLFIGIILILVOKLQSPDMGNGNESSYFSCVQKCYC--KPOAQHSCMKMSE 370
QY 853 LRSI-----AGLTFLGLITWG--FAFFAWGPVNVNT--FMYLFAI-FNTLOGFFIFIFYCV- 902
Db 371 LSTITLRLARSTLLILPLFGIHVTVFAFSPENVSKRERLIVFELGLSGFQGVVAVLYCFL 430
QY 903 ---AKENVKQWRRYLCCKGLRLAENSQDWS-----KTATNGLKKQTVNQGVSSSSNSLQSS 955
Db 431 NGEVQAEIKRKRWSW----KVNRYFTMDFKRHPHSLASSGVNGTQLSTLSKSSQLRMS 486
QY 956 S 956
Db 487 S 487

RESULT 25

US-08-855-213-21
; Sequence 21, Application US/08855213
; Patent No. 5892004
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 5892004io
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR
; TITLE OF INVENTION: PREPARING SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,213
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: 25-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 495 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-855-213-21

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Query Match      4.38; Score 231; DB 2; Length 495;
Best Local Similarity 22.68; Pred. No. 3e-10;
Matches 95; Conservative 74; Mismatches 146; Indels 106; Gaps 20;

QY 596 LGRNGRGWSD-----NGCSVKDRRLNETICTGSHLTSGVLLDLRTSVLPQAQMMAL 649
Db 113 VGRNCTEDGHWSEPPHYFDACGDDYE-----PESGDQDYYVLSV 152
QY 650 TTTYICGGLSSIFSLVTLVYIAFEKIR--RDYPSKILIQCAALLLLNLVLLDSWIA 707
Db 153 KALYTVGYSTSLATLTAMVILCRFKLCHTRNF---IHMNLFVSFMLRAISVFIKDWI- 208
QY 708 LYKMOGL-----CISVAVELHYFLLVSTWGLCAFHMYLALVKVENTYIRKYILK 758
Db 209 LYAEQDSSHCFVSTVECKAVWFFHYCVVSNFVLFIEGLYLTLLVETFEFPE-RRIFYW 267
QY 759 FCIVGWGPVAVVVTI--ILTISPONYGSGYKFPNGSPDDEFWNNNN--AVFYI---TV 811
Db 268 YTIIGNGTPTVCVTVWAVLRLYFDDAG-----CWDMDNSTALWVVIKGPV 312
QY 812 VGYFCVIFLLNVSMFIVVL-----VOLCRKKKKQLGAQRKTSIQD 852
Db 313 VGSIMVNFVLFIGIIIIIVQKLQSPDMGNGNESSIYFSCVKCYC--KQRAQQHSCMKSE 370
QY 853 LRSI---AGLTFLGLITWG--FAFFANGPVNVT--FMVLFAT-FNTLOGFFIFIFYCV- 902
Db 371 LSTITLRLARSTLLIPLFGIHYTVFAFSPENVSKRERLVFELGLSGFQGFVAVLYCFL 430
QY 903 ---AKENVKOWRRYLCGKRLRLAENSOWS-----KTATNGLKKQTVNQGVSSSSNSLOSS 955
Db 431 NSEVQAEIKRKRSW---KVNRYFTMDFKHRHPSLASSGVNGGTQLSILSKSSQLRMS 486
QY 956 S 956
Db 487 S 487
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Search completed: May 23, 2002, 07:38:04
Job time: 164 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2002, 07:36:21 ; Search time 25.95 Seconds
(without alignments)
3843.573 Million cell updates/sec

Title: US-09-731-657-2
Perfect score: 5352
Sequence: 1 SQPEDASGRCAQRFSTLSE.....GRMALRRTSKRGLHFIEQM 1038

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

PIR_71:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	536.5	10.0	1283	2	T18394 latrophilin-3, spl
2	536.5	10.0	1351	2	T18409 latrophilin-3, spl
3	536.5	10.0	1512	2	T18392 latrophilin-3, spl
4	536.5	10.0	1580	2	T18407 latrophilin-3, spl
5	536	10.0	1459	2	T17186 latrophilin-3, spl
6	536	10.0	1527	2	T17198 CL3AA protein - ra
7	534	10.0	1274	2	T18391 latrophilin-3, spl
8	534	10.0	1342	2	T18405 latrophilin-3, spl
9	534	10.0	1450	2	T18382 latrophilin-3, spl
10	534	10.0	1503	2	T18389 latrophilin-3, spl
11	534	10.0	1571	2	T18395 latrophilin-3, spl
12	533.5	10.0	1240	2	T18393 latrophilin-3, spl
13	533.5	10.0	1308	2	T18408 latrophilin-3, spl
14	532	9.9	1273	2	T17188 CL3AC protein - ra
15	532	9.9	1341	2	T17200 CL3BC protein - ra
16	531.5	9.9	1407	2	T18381 latrophilin-2 (spl
17	531.5	9.9	1550	2	T14327 alpha-latrophilin r
18	531	9.9	1231	2	T18390 latrophilin-3, spl
19	531	9.9	1299	2	T18398 latrophilin-3, spl
20	528.5	9.9	1465	2	T18384 latrophilin-2 (spl
21	527.5	9.9	1453	2	T18386 latrophilin-2 (spl
22	526	9.8	1422	2	T18383 latrophilin-2, spl
23	525	9.8	1230	2	T17187 CL3AB protein - ra
24	525	9.8	1298	2	T17199 CL3BB protein - ra
25	525	9.8	1420	2	T18385 latrophilin-2 (spl
26	522	9.8	1478	2	T18388 latrophilin-2 (spl
27	520.5	9.7	1384	2	T18366 latrophilin-2, spl
28	519.5	9.7	1435	2	T18387 latrophilin-2, spl
29	518	9.7	1341	2	T18301 latrophilin-2, spl

30	517	9.7	1582	2	T15308 hypothetical prote
31	515	9.6	1399	2	T18370 latrophilin-2 (spl
32	514	9.6	1397	2	T18377 latrophilin-2 (spl
33	512.5	9.6	1356	2	T18367 latrophilin-2 (spl
34	511.5	9.6	1354	2	T18375 latrophilin-2 (spl
35	510	9.5	1466	2	CL1AA protein - ra
36	510	9.5	1471	2	CL1BA protein - ra
37	508.5	9.5	1412	2	latrophilin-2 (spl
38	506	9.5	1369	2	latrophilin-2 (spl
39	506	9.5	1463	2	CL2AC protein - ra
40	505	9.4	1467	2	T18411 latrophilin-1, bra
41	505	9.4	1472	2	T18413 latrophilin-1, bra
42	503	9.4	1420	2	T17158 CL2AB protein - ra
43	500.5	9.4	1478	2	T17185 CL2BC protein - ra
44	498	9.3	1487	2	T14324 alpha-latrophilin r
45	497.5	9.3	1435	2	T46611 CL2BB protein - ra
46	494.5	9.2	1452	2	T17157 CL2AA protein - ra
47	494	9.2	1510	2	T17145 CL1BB protein - ra
48	494	9.2	1515	2	T17156 CL2BA protein - ra
49	489	9.1	1467	2	T17160 leucocyte antigen
50	461	8.6	742	2	I37225 seven-pass transme
51	457	8.5	3034	2	T14119 hypothetical prote
52	452	8.4	1014	2	T18759 probable hormone r
53	438	8.2	886	2	A57172 brain-specific ang
54	409	7.6	1572	2	T00027 brain-specific ang
55	403	7.5	1522	2	T00028 MEGF2 protein - nu
56	397	7.4	1364	2	T00250 brain-specific ang
57	379.5	7.1	1584	2	T00026 hypothetical prote
58	260.5	4.9	984	2	T00326 pituitary adenylat
59	233	4.4	467	2	T00616 pituitary adenylat
60	231	4.3	495	2	S36114 corticotropin-rele
61	230	4.3	415	2	I58144 pituitary adenylat
62	228.5	4.3	513	2	S47631 pituitary adenylat
63	227.5	4.3	525	2	JN0902 pituitary adenylat
64	225	4.2	415	2	S39535 corticotropin-rele
65	224.5	4.2	798	2	T34248 hypothetical prote
66	223.5	4.2	381	2	S34449 pituitary adenylat
67	223.5	4.2	459	2	JH0594 vasoactive intesti
68	223	4.2	495	2	S39061 pituitary adenylat
69	220	4.1	523	2	S39060 pituitary adenylat
70	215	4.0	375	2	I38879 corticotropin rele
71	210.5	3.9	444	2	A48260 corticoliberin rec
72	209	3.9	411	2	A5610 corticotropin-rele
73	208.5	3.9	460	2	JC2194 vasoactive intesti
74	208.5	3.9	495	2	JC2195 vasoactive intesti
75	208	3.9	431	2	I49149 CRF receptor - mou
76	205	3.8	449	2	S16319 secretin receptor
77	204	3.8	430	2	A56726 corticoliberin rec
78	201.5	3.8	431	2	I49279 sauvagine/corticot
79	199.5	3.7	463	2	A46172 glucagon-like pept
80	198.5	3.7	464	2	I60194 calcitonin-like re
81	193	3.6	644	2	E88487 protein CL3B9.4 [i
82	190	3.6	1817	2	T34249 hypothetical prote
83	189	3.5	490	2	S34486 calcitonin recepto
84	188.5	3.5	437	2	JU0185 PACAP/VIP receptor
85	188	3.5	463	2	S71624 glucagon-like pept
86	186	3.5	550	2	A57519 parathyroid hormon
87	185	3.5	440	2	JC2532 secretin receptor
88	185	3.5	585	2	A39286 parathyroid hormon
89	184.5	3.4	461	2	JC2477 calcitonin recepto
90	182	3.4	479	2	S33746 calcitonin recepto
91	182	3.4	593	2	A49191 parathyroid hormon
92	181.5	3.4	463	2	I84494 glucagon-like pept
93	181.5	3.4	1161	2	S57180 probable membrane
94	181	3.4	591	2	I54195 parathyroid hormon
95	180	3.4	589	2	I59297 parathyroid hormon
96	180	3.4	744	2	E86255 hypothetical prote
97	179	3.3	227	2	T47186 hypothetical prote
98	178	3.3	478	2	A37430 calcitonin recepto
99	176	3.3	482	2	A39285 calcitonin recepto
100	175.5	3.3	437	2	S39069 vasoactive intesti

ALIGNMENTS	
RESULT 1	
Tl8394	
latrophilin-3, splice variant abbb, brain-specific - bovine	
C:Species: Bos primigenius taurus (cattle)	
C:date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000	
C:Accession: Tl8394	
R:Matsushita, H.; Lelianova, V.G.; Ushkaryov, Y.A.	
FEBS Lett. 443, 348-352, 1999	
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with diff	
A:Reference number: Z18869; MUID:99148828	
A:Accession: Tl8394	
A:Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1-1283 <MAT>	
A:Cross-references: EMBL:AF111090; NID:g4164062; PID:g4164063; PIDN:AAD05326.1	
C:Superfamily: alpha-latotoxin receptor, calcium-independent	
C:Keywords: alternative splicing; G protein-coupled receptor	
Query Match 10.0%; Score 536.5; DB 2; Length 1283;	
Best Local Similarity 23.7%; Pred. No. 3.9e-23;	
Matches 206; Conservative 124; Mismatches 334; Indels 205; Gaps 30;	
QY 260 LQPIVCLADHPGPPFSSSSQSIPIVPRATVLSQVPKATSFAPDPDYPVTHNVPSPIGE 319	
DB 409 ISPIHLSDSLERPPVREISTGTGCTGTTTTLRTTT-----WSPGRSTTPSVSGR 462	
QY 320 IQPLSPQSPAPIASSPAIDMPQSETISSPMPQTHVSGTPPPVKASFSS----- 368	
DB 463 RNRSTSTP-----SPAIEVLNDI-----TTHVPSASPOIPALEESCEAVEAREIMW 508	
QY 369 -----PTVSAPANVNT--TSAP-----PVQTDIVNTSSISDLENQVLOMEKALS 410	
DB 509 FKTRQGMOKPCPAGTIGVSTYLCLAPDGIWDPQGDLSNCS--SPWNHITOKLKS-- 564	
QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440	
DB 565 -GETAANTARELAEQTRNHLNAGDITYSVRAMDQVLGLDVLRLNLTGGKDSAAARSLNK 623	
QY 441 -----AQRLLKVDDIGLQNFNS-----TTISLTPSLSALAVIR-----VNAS 479	
DB 624 LQKRERSCRAYQAMVETVNNL-LQPOLNARWDLTTSQDLRAATMLDITVEESAFVLAD 682	
QY 480 SFNTTFFVAQDPANLQVLETOAPENSIGTITLPSL-----MNNLPAHDMELASR 530	
DB 683 NLLKTDIVRENTDNIQLEVARLSTEGNLDLKFPENTGHSTIQLSANTLKQNGRNGEIR 742	
QY 531 VQFNFFET--PALFQDPSPLENLSL-----ISYVISSSVANLTVRN-----LTR 571	
DB 743 VAFVLYNNLGPYL-----STENASMKLGTEAMSTNHSVIVNSPVITAAINKEFSNKVYLAD 798	
QY 572 NVTYTLKHINPSODELTVCVFDWDLGRNGGWSGDSVCKDRRLNETICTCSHLTSFG 631	
DB 799 PVVFTVKHIKQSEENFPNCSEFSWYSKRTMTGYWSTQGCRLLTNTKTHHTTCCSNHLTNFA 858	
QY 632 VLL---DLSRSTSVLPQAOMMALFTFYIGCGLSISFLSVTLVTVIAFEKIRRDYPSKILIQ 688	
DB 859 VLMAHVEKHSADV--HDLLDVITWVGILLSVCLLICITFCFFRGLQSD--RNTIHKN 915	
QY 689 LCAALLLNLFLL-----DSWIALYKMOGLCISAVFLHYFLVSTTWGLFAFHYLA 743	
DB 916 LCISLFAELLFLIGINRDTQPIA-----CAVFAALLHFFFLAFTWFMLEGVQLYIM 968	
QY 744 LKVPNT--YIRKYILKFCIVGWGVPVAVVTIILTISPDNYGLGSYKFPNGSPDDFCWI 801	
DB 969 LVEFESEHSRRKY---FYLVGMPALIVAVSAADYRSIG-----TDKVCWL 1014	
QY 802 NNNAVFYITVGVGFCVIFLLNYSMTFVVLVOLCRIK--KKQLGAQRKTSIQDLR----- 854	
DB 1015 RLDYTFIWSFIGPATLIIMLVIFLGIALYKMFHHTAILKPESCCLDNINVEDNRPFIKS 1074	

ALIGNMENTS	
RESULT 2	
Tl8409	
latrophilin-3, splice variant bbbb, brain-specific - bovine	
C:Species: Bos primigenius taurus (cattle)	
C:date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000	
C:Accession: Tl8409	
R:Matsushita, H.; Lelianova, V.G.; Ushkaryov, Y.A.	
FEBS Lett. 443, 348-352, 1999	
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with di	
A:Reference number: Z18869; MUID:99148828	
A:Accession: Tl8409	
A:Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1-1351 <MAT>	
A:Cross-references: EMBL:AF111096; NID:g4164074; PID:g4164075; PIDN:AAD05332.1	
C:Superfamily: alpha-latotoxin receptor, calcium-independent	
C:Keywords: alternative splicing; G protein-coupled receptor	
Query Match 10.0%; Score 536.5; DB 2; Length 1351;	
Best Local Similarity 23.7%; Pred. No. 4.2e-23;	
Matches 206; Conservative 124; Mismatches 334; Indels 205; Gaps 30;	
QY 260 LQPIVCLADHPGPPFSSSSQSIPIVPRATVLSQVPKATSFAPDPDYPVTHNVPSPIGE 319	
DB 477 ISPIHLSDSLERPPVREISTGTGCTGTTTTLRTTT-----WSPGRSTTPSVSGR 530	
QY 320 IQPLSPQSPAPIASSPAIDMPQSETISSPMPQTHVSGTPPPVKASFSS----- 368	
DB 531 RNRSTSTP-----SPAIEVLNDI-----TTHVPSASPOIPALEESCEAVEAREIMW 576	
QY 369 -----PTVSAPANVNT--TSAP-----PVQTDIVNTSSISDLENQVLOMEKALS 410	
DB 577 FKTRQGMOKPCPAGTIGVSTYLCLAPDGIWDPQGDLSNCS--SPWNHITOKLKS-- 632	
QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440	
DB 633 -GETAANTARELAEQTRNHLNAGDITYSVRAMDQVLGLDVLRLNLTGGKDSAAARSLNK 691	
QY 441 -----AQRLLKVDDIGLQNFNS-----TTISLTPSLSALAVIR-----VNAS 479	
DB 692 LQKRERSCRAYQAMVETVNNL-LQPOLNARWDLTTSQDLRAATMLDITVEESAFVLAD 750	
QY 480 SFNTTFFVAQDPANLQVLETOAPENSIGTITLPSL-----MNNLPAHDMELASR 530	
DB 751 NLLKTDIVRENTDNIQLEVARLSTEGNLDLKFPENTGHSTIQLSANTLKQNGRNGEIR 810	
QY 531 VQFNFFET--PALFQDPSPLENLSL-----ISYVISSSVANLTVRN-----LTR 571	
DB 811 VAFVLYNNLGPYL-----STENASMKLGTEAMSTNHSVIVNSPVITAAINKEFSNKVYLAD 866	
QY 572 NVTYTLKHINPSODELTVCVFDWDLGRNGGWSGDSVCKDRRLNETICTCSHLTSFG 631	
DB 867 PVVFTVKHIKQSEENFPNCSEFSWYSKRTMTGYWSTQGCRLLTNTKTHHTTCCSNHLTNFA 926	
QY 632 VLL---DLSRSTSVLPQAOMMALFTFYIGCGLSISFLSVTLVTVIAFEKIRRDYPSKILIQ 688	
DB 927 VLMAHVEKHSADV--HDLLDVITWVGILLSVCLLICITFCFFRGLQSD--RNTIHKN 983	

QY 689 LCAALLLLLVFL-----DSWIALYKMGGLCISVAVFLHYFLVLLVFTWGLFAFHMYLA 743
Db 984 LCISLFAELLFLIGINRTDPIA-----CAVFAALLHFFFLAAFTWMFLGVQLYIM 1036
QY 744 LKVFNT--YIRKYLKFCVGVPAVVVILLISPDNYGLSGYKGPNGSPDDFCWI 801
Db 1037 LVEVFESHSRRY---FYLVGYGMPALIVAVSAADYRSYG-----TDKVCWL 1082
QY 802 NNNAVFIYTVGVFCVIFLLNVSMFIVVLVOLCRICK--KKOLGAQRKTSIODLR----- 854
Db 1083 RLDTYFIWFIGPATLIIMLVNIFGLTALYKMFHHTAILKPESGCLDNTINEDNRFPIKS 1142
QY 855 ---SIAGLFLGITWGFAPFANGPVNVTFMYLFAFNLTQGLFFIFCYCAKENVRKOW 911
Db 1143 WVGATALLCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFHCVLQKKVKEY 1202
QY 912 RRYL---CC-----GKRLAENDSWKSTATNGLKKOTVNOGVSS 948
Db 1203 GKCLRTHCCSGRSTESSIGSKTSGRTPGRTGSGSRIRRMWMDTVRKQSESSFITGD 1262
QY 949 SNSLOSSNSTNTLLVNNDCSVHASN 977
Db 1263 INSSASLRGAMANHLISNALLRPHGTNN 1291
RESULT 3
T18392
latrophilin-3, splice variant abbf, brain-specific - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18392
R: Matsushita, H.; Lellanova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A: Title: The latrophilin family: multiply spliced G protein-coupled receptors with diffe
A: Reference number: Z18869; MUID: 99148828
A: Accession: T18392
A: Status: preliminary; translated from GB/EMBL/DBDJ
A: Molecule type: mRNA
A: Residues: 1-1512 <MAT>
A: Cross-references: EMBL: AF111088; NID: 94164058; PID: 94164059; PIDN: AAD05324.1
C: Superfamily: alpha-latotoxin receptor, calcium-independent
C: Keywords: alternative splicing; G protein-coupled receptor
Query Match 10.0%; Score 536.5; DB 2; Length 1512;
Best Local Similarity 23.7%; Pred. No. 4.9e-23;
Matches 206; Conservative 124; Mismatches 334; Indels 205; Gaps 30;
QY 260 LQDPIVCLADHPGPPFSSQSIPVVPVPRATVLSQVPRKATSAEPDPYSPVTHNVPSPIGE 319
Db 409 ISPPHLSDLRPPVREISTGTPLGTGTTTTLRTTT-----WSPGRSTTPSVSGR 462
QY 320 IQPLSPQSPASPIASSPAIDMPPQSETISSPMQTHVSGTPPVKASFS----- 368
Db 463 RNRSTSTP-----SPAIEVLNDI-----TTHVPSASQIPALEESCEAVEAREINMW 508
QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSIDLENQVLOMEKALS 410
Db 509 FKTRQGMQKQPCPAGTIGVSTYLCLAPDGIWDPQGDLSNCS--SPWVNHTQKLKS-- 564
QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440
Db 565 -GETAANIARELAETRNHLNAGDITYSVRAMQVLGLDVLQRLNLTGPKGDSAAARSLNK 623
QY 441 -----AQRLLKVDDIGLQNFN-----TTISLTSPSLAVTR-----VNAS 479
Db 624 LOKRERSRAYVOAMVETVNNL-LQPOALNAWRDLTTSQOLRAATMLDITVEESAFVLAD 682
QY 480 SFNFTTFFVAQDPANLQVSLQETQAPENSIGFTITLPSL-----MNNLPAHDMELASR 530
Db 683 NLLKTDIVRENTDNQLQELVARLSTEGNLEDKLPENFGHGSTIQLSANTLKGNGRNGEIR 742
QY 531 VQNFET--PALFQDPSLENLSL-----ISYVISSSVANLATVRN-----LTR 571

Db 743 VAEVLVNNLGPYL-----STENASMKLGMTAMSTNHSVIVNSPVITAAINKEFGSNKVYLAD 798
QY 572 NVTVLTKHINPSONDELTVRCVFDLGRNGRGGSDNGSVKDRRLNRNETICTCGSHITSFG 631
Db 799 PVVFTVKHKQISENENFNCPSFWSYSKRTMTGYWSTQGCRLTTNKTHTTSCNHLTNEA 858
QY 632 VLL---DLSRTSVLPAOMMALTFTYICGGLSSIFSLSVTLVTVIAFEKIRRDYPSKILIQ 688
Db 859 VLMHAEVKHSDAV--HDLILLDVITWVIGILLSVCLLCIFTCFPGGLQSD--RNTIHN 915
QY 689 LCAALLLLLVFL-----DSWIALYKMGGLCISVAVFLHYFLVLLVFTWGLFAFHMYLA 743
Db 916 LCISLFAELLFLIGINRTDPIA-----CAVFAALLHFFFLAAFTWMFLGVQLYIM 968
QY 744 LKVFNT--YIRKYLKFCVGVPAVVVILLISPDNYGLSGYKGPNGSPDDFCWI 801
Db 969 LVEVFESHSRRY---FYLVGYGMPALIVAVSAADYRSYG-----TDKVCWL 1014
QY 802 NNNAVFIYTVGVFCVIFLLNVSMFIVVLVOLCRICK--KKOLGAQRKTSIODLR----- 854
Db 1015 RLDTYFIWFIGPATLIIMLVNIFGLTALYKMFHHTAILKPESGCLDNTINEDNRFPIKS 1074
QY 855 ---SIAGLFLGITWGFAPFANGPVNVTFMYLFAFNLTQGLFFIFCYCAKENVRKOW 911
Db 1075 WVGATALLCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFHCVLQKKVKEY 1134
QY 912 RRYL---CC-----GKRLAENDSWKSTATNGLKKOTVNOGVSS 948
Db 1135 GKCLRTHCCSGRSTESSIGSKTSGRTPGRTGSGSRIRRMWMDTVRKQSESSFITGD 1194
QY 949 SNSLOSSNSTNTLLVNNDCSVHASN 977
Db 1195 INSSASLRGAMANHLISNALLRPHGTNN 1223
RESULT 4
T18407
latrophilin-3, splice variant bbbf, brain-specific - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18407
R: Matsushita, H.; Lellanova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A: Title: The latrophilin family: multiply spliced G protein-coupled receptors with di
A: Reference number: Z18869; MUID: 99148828
A: Accession: T18407
A: Status: preliminary; translated from GB/EMBL/DBDJ
A: Molecule type: mRNA
A: Residues: 1-1580 <MAT>
A: Cross-references: EMBL: AF111094; NID: 94164070; PID: 94164071; PIDN: AAD05330.1
C: Superfamily: alpha-latotoxin receptor, calcium-independent
C: Keywords: alternative splicing; G protein-coupled receptor
Query Match 10.0%; Score 536.5; DB 2; Length 1580;
Best Local Similarity 23.7%; Pred. No. 5.2e-23;
Matches 206; Conservative 124; Mismatches 334; Indels 205; Gaps 30;
QY 260 LQDPIVCLADHPGPPFSSQSIPVVPVPRATVLSQVPRKATSAEPDPYSPVTHNVPSPIGE 319
Db 477 ISPPHLSDLRPPVREISTGTPLGTGTTTTLRTTT-----WSPGRSTTPSVSGR 530
QY 320 IQPLSPQSPASPIASSPAIDMPPQSETISSPMQTHVSGTPPVKASFS----- 368
Db 531 RNRSTSTP-----SPAIEVLNDI-----TTHVPSASQIPALEESCEAVEAREINMW 576
QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSIDLENQVLOMEKALS 410
Db 577 FKTRQGMQKQPCPAGTIGVSTYLCLAPDGIWDPQGDLSNCS--SPWVNHTQKLKS-- 632
QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440

QY	308	PV-----THNVSPICEIOPLSPQSPAPIASSPAIDMPQSEITISSPMPQTHVSGTTP	360
DB	457	PSLPGRRNRSTSTSP--AIEVLDVTHLPSAASQIPAMEESCEAVEAREIMWFMTKROGQ	514
QY	361	PVKASFSPPTVS-----APANVTTTAPPVQTDIVNTSSISDLENQVLOMEKALSLS	413
DB	515	VAKQSCPAGTTIGVSYLCLAPDGIWDPOGP---DLSNCS--SPWVNHITQKLKS---GE	565
QY	414	LEPNLAGEMINQVSRLLHS-----PPDMLAPL-----	440
DB	566	TAANIARELAQTRNHLNAGDITYSVRAMDQVLGLDVLQRLNLTGGKDSAAARSLNK	625
QY	441	-----AQRLLKVVDDIGLQNFN-----TTISLTSPSLALAVIR---VNASSEN	482
DB	626	RESCRAYVOAMVETVNNL-LQPOALNAWRDLTTSQDLRAATMLDVTVEESAFVLAD	684
QY	483	TTTFVAQDPANLQVLETOAPENSIGTITLPSL-----MNNLPAHDMELASRVQF	533
DB	685	KTDIVRENTDNIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKONGRNGELRVAF	744
QY	534	NFFET--PALFQDPSLENLSL-----ISYVISSSVANLTVRN-----LFRNVT	574
DB	745	VLYNNGPYL---STENASMKLGTEAMSTNHSVIVNSPVIATAINKFNSKVYLADPVV	800
QY	575	VTLKHINPSQDELTVRCVFWDLGRNGRGWSDNGSVKDRRLNETICTCSHLTSFGVLL	634
DB	801	FTVKHIQSEENFNPCSEFWSYKRTMTGYSTQGRLLTTNKTHCTSCNHLTNFAVLM	860
QY	635	---DLRSTSVLPAQMMALFTIYICGLSSIFLSVTLVTVIAFEKIRRDYPSKILIQ	691
DB	861	AHVEVKHSDAV--HDLLLDVITWVGILLSLVCLLCIIFTCFFRGLQSD--RNTIHNLCI	917
QY	692	ALLNLNVFL-----DSWIALYKMGGLCISVAVFLHYFLVLSFTWMGLEAFHMYLALVK	746
DB	918	SLFAELLFLIGINRTDQPIA-----CAVEAALLHFFFLAAFTWMFLEGVQLYIMLVE	970
QY	747	VFT--YTRKYTLKFCIVGWGPVAVVITLITSPDNYGLSGYKGFNGSPDDFCWINNN	804
DB	971	VFSEHSRKY---FYLVGYPALIVAVSAADVRSYG-----TDKVCWLRLD	1016
QY	805	AVFYTVVGYFCVIFLLNVSMFIVLVQLCRICK--KKOLGAQRKTSIQDLRSIAGTLFL	862
DB	1017	TYFWSFGPATLIIMNLVIFLGIALYKMFHTAILKPESGCLDNITKSWVIGAI--LLCL	1075
QY	863	LGITWGAFFAWGPNVTFMYLFAIFNTLQGFIFIFCVAKENVRKQW---RRYLCCG	918
DB	1076	LGLTWAFGLMYINESTVMAYLFTIFNSLQGMFIFIFHCVLQKVRKEYGKCLRTHCCSG	1135
QY	919	KL-----RLAENS-----WSKTATNGLKQTVNOGVSSSSNSLQSS	955
DB	1136	KSTESSIGSKTSGSRTPGRYSTGSQSRIRRMWNTD---VRKQSESSFITGDIN---S	1187
QY	956	SNSTNTSTLLVN-NDCSVHAS--GNGNASTERNGVSFVSQNGD	995
DB	1188	SASLNREGLLNARDTSVMDTLPNGN-----HGNSYSIAGGE	1225
RESULT 6			
T17198			
CL3BA protein - rat			
C:Species: Rattus norvegicus (Norway rat)			
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000			
C:Accession: T17198			
R:Sugita, S.; Ichchenko, K.; Khvotchev, M.; Sudhof, T.C.			
submitted to the EMBL Data Library, July 1998			
A:Description: CL family.			
A:Reference number: 218712			
A:Accession: T17198			
A>Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-1527 <SUG>			
A:Cross-references: EMBL:AF081157; NID:g3695140; PID:g3695141; PIDN:AAC62663.1			
C:Superfamily: alpha-latrototoxin receptor, calcium-independent			

QY	633	-GETAANIARELAQTRNHLNAGDITYSVRAMDQVLGLDVLQRLNLTGGKDSAAARSLNK	691
DB	441	-----AQRLLKVVDDIGLQNFN-----TTISLTSPSLALAVIR---VNAS	479
QY	692	LQKRERSCRAYVOAMVETVNNL-LQPOALNAWRDLTTSQDLRAATMLDVTVEESAFVLAD	750
DB	480	SFNTTTFVAQDPANLQVLETOAPENSIGTITLPSL-----MNNLPAHDMELASR	530
QY	751	NLLKTDIVRENTDNIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKONGRNGEIR	810
DB	531	VQNFET--PALFQDPSLENLSL-----ISYVISSSVANLTVRN-----LFR	571
QY	811	VAFVLYNNGPYL---STENASMKLGTEAMSTNHSVIVNSPVIATAINKFNSKVYLAD	866
DB	572	NVTYTLKHINPSQDELTVRCVFWDLGRNGRGWSDNGSVKDRRLNETICTCSHLTSFG	631
QY	867	PVFTVKHIQSEENFNPCSEFWSYKRTMTGYSTQGRLLTTNKTHCTSCNHLTNFA	926
DB	632	VLL---DLRSTSVLPAQMMALFTIYICGLSSIFLSVTLVTVIAFEKIRRDYPSKILIQ	688
QY	927	VMAHVEVKHSDAV--HDLLLDVITWVGILLSLVCLLCIIFTCFFRGLQSD--RNTIHN	983
DB	689	LCAALLNLNVFL-----DSWIALYKMGGLCISVAVFLHYFLVLSFTWMGLEAFHMYLA	743
QY	984	LCISLFAELLFLIGINRTDQPIA-----CAVEAALLHFFFLAAFTWMFLEGVQLYIM	1036
DB	744	LVKVFT--YTRKYTLKFCIVGWGPVAVVITLITSPDNYGLSGYKGFNGSPDDFCWI	801
QY	1037	LVEFESEHSRKY---FYLVGYPALIVAVSAADVRSYG-----TDKVCWL	1082
DB	802	NNNAVEYTVVGYFCVIFLLNVSMFIVLVQLCRICK--KKOLGAQRKTSIQDLR-----	854
QY	1083	RLDTYFWSFGPATLIIMNLVIFLGIALYKMFHTAILKPESGCLDNINYEDNRPEIKS	1142
DB	855	---SIAGTLFLGLTWGFAFWGPNVTFMYLFAIFNTLQGFIFIFCVAKENVRKQW	911
QY	1143	-AVIGAIALLCLGLTWAFGLMYINESTVMAYLFTIFNSLQGMFIFIFHCVLQKVRKEY	1202
DB	912	RYL---CC-----GKURLAENSQWSTATNGLKKOTVNOGVSSS	948
QY	1203	GKURTHCCSGRSTESSIGSKTSGSRTPGRYSTGSQSRIRRMWNTVTRKQSESSFITGD	1262
DB	949	SNLSQSSNSTNTLLVNNDCSVHASGN	977
QY	1263	INSSASLNKRGAMANHLISNALLRPHGTNN	1291
RESULT 5			
CL3BA protein - rat			
C:Species: Rattus norvegicus (Norway rat)			
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000			
C:Accession: T17186			
R:Sugita, S.; Ichchenko, K.; Khvotchev, M.; Sudhof, T.C.			
submitted to the EMBL Data Library, July 1998			
A:Description: CL family.			
A:Reference number: 218712			
A:Accession: T17186			
A>Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-1459 <SUG>			
A:Cross-references: EMBL:AF081154; NID:g3695134; PID:g3695135; PIDN:AAC62660.1			
Superfamily: alpha-latrototoxin receptor, calcium-independent			
Query Match 10.0%; Score 536; DB 2; Length 1459;			
Best Local Similarity 24.7%; Pred. No. 5e-23;			
Matches 218; Conservative 131; Mismatches 344; Indels 190; Gaps 35;			
QY	248	SSPEELGKLCQDLQPIVGLADHPGPPFPSSQSIQVVPATVLSQVPKATSAEPDPYS	307
DB	398	SGPVHGVQSVY-ISPIHLDSLDLPPVPGISITGPIGLMGSTTTTTLRTTWNLGRSTT	456

R;Matsushita, H.; Lelianova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A;Title: The latrophilin family: multiply spliced G protein-coupled receptors with di
A;Reference number: Z18869; MUID:99148828
A;Accession: T18391
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1274 <MAT>
A;Cross-references: EMBL:AF111087; NID:q4164056; PID:q4164057; PIDN:AAD05323.1
C;Superfamily: alpha-latrotoxin receptor, calcium-independent
C;Keywords: alternative splicing; G protein-coupled receptor

Query Match	10.08;	Score 534;	DB 2;	Length 1274;
Best Local Similarity	23.9%;	Pred. No. 5.4e-23;		
Matches	206;	Conservative 124;	Mismatches 333;	Indels 198; Gaps 30;
QY	260	LQDPIVLADHPGRGPPSSSOSIPVPRATVLSQVFKATSFAPDPDYSPTVHNVPSPIGE	319	
DB	409	ISPIIHLDSLERPPVREISWTGLGCGSTTTTLRTTT-----WSPGRSTTPSVSGR	462	
QY	320	IQPLSQPSAPIASSPAIDMPQSETISPMPTQHSVGTTPPPVKASFSS-----	368	
DB	463	RNRSTSTP-----SPAIEVLNDI-----TTHVPSASPOIPALEESCEAVEAREIMW	508	
QY	369	-----PTVSAPANVT--TSAP-----PVQTDIVNTSSIDLENQVLOMEKALS	410	
DB	509	FKTRQCGMAKQPCPAGHIGVSTYLCCLAPDGDWPGPDLSNCS--SPWYNHITQKLKS--	564	
QY	411	LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL-----	440	
DB	565	-GETAANIARELAETQRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGKDSAAARSLNK	623	
QY	441	-----AQRLKVVDDIGLQLFNSN-----TWISLSPSLALAVIR-----VNAS	479	
DB	624	LQKRERSCRAYQGMVETVNNL-LQPALNAWRDLTTSQDLRAATMLLDTVEESAFLAD	682	
QY	480	SPNTTTFVAQDPANLQVLSLETOAPENSIGITTLPSL-----MNNLPAHDMELASR	530	
DB	683	NLLKTDIVRENTDNIQLEVARLSTEGNLEDLKFPENTCHGSTIQLSANTLKQNGRGEIR	742	
QY	531	VOFNPFET--PALFQDPSLENLSL-----ISYVISSVANLTVRN-----LFR	571	
DB	743	VAFVLNNLGPYL-----STENASMKLGEAMSTNHSVIVNTPVITAAINKEEFSNKVYLAD	798	
QY	572	NYVTVLKHINPSODELTVCRVFDLGRNGRGWGSDNGCSVKDRRLNETICFCSHLTSG	631	
DB	799	PVVFETVKHIKQSEENFNPCNSFWSYSKRTWTGYWSTQGRLLTTNKTHTTCSNHLTNTA	858	
QY	632	VLL-----DLSETSVLPQAOMALTFITYTGGLSSTFLSVTLTYTIAFEKIRRDYPSKILQ	688	
DB	859	VLMAHVEVHKSDAV--HDLLDVITWYGIILSLVCLLCICITFCFCFRGLQSD--RNTIHK	915	
QY	689	LCAALLMLLVLL-----DSWIALYKMOGLCISAVFVHLLVSWFMGLEAFHMYLA	743	
DB	916	LCISLFAVELLEFLIGNRDTQPTA-----CAVFAALLHEFFTLAAFTWFMLEGVOLYIM	968	
QY	744	LVKVNT--YIRKYLKFCIVGKVPVAVVYTIILTISPDNYGLGSGYKFPNGSPDDFCWI	801	
DB	969	LVEVFESEHSRRKY----FVLGVGYMPALIVAVSAADVRSYG-----TDKVCWL	1014	
QY	802	NNNAVETYTVVCYFCVIFLLNYSMFIVVLVOLCRICK--KQLGAQRKYSTODLRSIAGL	859	
DB	1015	RLDTYFVWSFGPATLIIMLVIFLGIALYKMFHHTAILALPESCCLDNIKSWVIGAI--L	1073	
QY	860	TFLGWTGFAFPWAGPVNVNTMYLEFAINFNTLQGGFFIFCYCVAKENVKRWRYL--C	916	
DB	1074	LCLLGLTWAFGLMYINESVIMAYLFTFNSLOGMFIIFHCVLQKVKKEYKCLRTHC	1133	
QY	917	C-----CKRLAENSWSKATNGLKKQTVNOCGVSSSSNSLQSS	956	
DB	1134	CSGRSTESSIGSKTSGSRTPGYRSTGSGSIRRMWMDTVRKQSESSFITGDINSASLN	1193	

Query Match	10.0%;	Score 536;	DB 2;	Length 1527;
Best Local Similarity	24.7%;	Pred. No. 5.3e-23;		
Matches 218;	Conservative 131;	Mismatches 344;	Indels 190;	Gaps 35;
QY	248	SSPEELGKLOCDLQDPVCLADHPRGPPFSSSQSIPVVPVATVLSQVFKATSAEPDPYS	307	
DB	466	SGPVHGVQSY-ISPPIHDSLDLERPVRGISTGPIGMGGTTTTTTLRTTTTTLNGLRSTT	524	
QY	308	PV-----THNVSPIGBIQIPLSPSPASPIASSPAIDMPQSEITSSPMPQTHVSGTTP	360	
DB	525	PSLPCRRNRKSTSPS-AIEVLDVTHLPSAASQIPAMEESCEAVEAIEIMWFKTRQOQ	582	
QY	361	PVKASFSEPTVS-----APANVNTSAPVQTDIVNTSSISDLNOVLQMEKALSLGS	413	
DB	583	VAKOSCPAGTIGVSTYCLAPDGIWDPQG-----DLSNCS--SPWVNHTOKLKS--GE	633	
QY	414	LEPNLAGMINQVSRLLHS-----PPDMLAPL-----	440	
DB	634	TAMIARELAEQTRNHLNAGDITYSVRAMDQVLGLDVQLRNLTPGGKDSAAARSLNKLOK	693	
QY	441	-----AQRLLKVVDDIGLQNFN-----TTISLTPSPLALAVIR-----VNASSEN	482	
DB	694	RESCRATVQAWVETVNNL-LQPQALNAREDLTSDQLRATMLLDTVEESAFVIALNLL	752	
QY	483	TTTFEVAQDPANQLVSLAQAPENSIGTITLPSL-----MNNLPAHDMELASRVQF	533	
DB	753	KTDIVRENTIOLEVARLSLTGNELEDLKFPEGTGHGSTITQLSANTLKGNGRGEIRVAF	812	
QY	534	NFFET--PALFQDPSELENL-----ISYVTSSSVANLTVRN-----LTRNVT	574	
DB	813	VLNNLGPYL-----STENASKMLGTEAMTNHNSVIVNSPVITAAINKEFSNKVYLADPVV	868	
QY	575	VTLLKHINPSODELTVRCVFDLGRNGRGGSVDNGSGVKDRRLNETICTCSHLTSFGVLL	634	
DB	869	FTVKHIKQSENFENPNCFSWSYKRTMTGYSTQGCRLLTNNKTHHTTCSCHLNTFAVILM	928	
QY	635	---DLRSTSVLPQAOMMALTFITYICGGLSIFLSVLTVTYIAEKIRRDYPSKILIQCA	691	
DB	929	AHVEVKHSDAV---HDLLDVITWVGILLVLCVLLCICITFCFFRGLOSD-RNTIHNLCI	985	
QY	692	ALLLLNLVFL-----DSWIALYKMQGLCISAVAEHLYFLVSPFTWGLAEFHYMLALVK	746	
DB	986	SLFVAELFLIGINRTDQPIA-----CAVFAALHFFFLAFTWFEGLVQLYIMLVE	1038	
QY	747	VFNT--YIRYILKFCIVGWGPVAVVVTIILTISPQNYGLSGYKFFPNSGPDDFCWINNN	804	
DB	1039	VFESHSRRRY---FYLGVGMPALIVAVSAADVRSYG-----TDKVCWLRLD	1084	
QY	805	AVFYITWVGFCVFLFLNVSFIVVLVOLCRKK--KKQLGAORKTSGIDLRSTIAGLTFL	862	
DB	1085	TYFIWFGPATLIILNIVPLGIALYKMFHHTAILKPSGGCLDNIKSWVIGATA-LLCL	1143	
QY	863	LGITWGAFFAWGPVNTFMYLFAIFNTLQGFIFIFYCVAKENVRKQW---RRLYLCG	918	
DB	1144	LGLTWAFGLMYINESTYIMAYLFWIFENSLOGMFIIFHCVLQKAKVREYQKCLRTHOCSG	1203	
QY	919	KL-----RLAENSD-----WSKTATNGLKKQTKVQGVSSSSNSLQSS	955	
DB	1204	KSTESSIGSKTSGSRTPRGYSTGQSRIIRMMWDT---VRKQSESSFITGDIN----S	1255	
QY	956	SNSTNSTTLLVN-NDCSVHAS--GNGNASTERNGVSVFQVONG	995	
DB	1256	SASLNREGLLNNAARDYSMDTLPNLGN---HGNSYSTAGGE	1293	

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RESULT 7
T18391
      splice variant abah, brain-specific - bovine
      ;Species: Bos primigenius taurus (cattle)
      ;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
      ;Accession: T18391

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QY 957 NSTNSTLLVNDSCSVHASN 977
Db 1194 RGAMANHLISNALLRPHGTNN 1214
RESULT 8
Ti18405
latrophilin-3, splice variant bbah, brain-specific - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18405
R:Matsushita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with different
A:Reference number: Z18869; MUID:99148828
A:Accession: T18405
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1342 <MAT>
A:Cross-references: EMBL:AF111093; NID:94164068; PID:94164069; PIDN:AA05329.1
C:Superfamily: alpha-latrototoxin receptor, calcium-independent

Query Match 10.0%; Score 534; DB 2; Length 1342;
Best Local Similarity 23.9%; Pred. No. 5.8e-23;
Matches 206; Conservative 124; Mismatches 333; Indels 198; Gaps 30;

QY 260 LQPIVCLADHGRPPSSOSIPVPRATVLSQVPKATSAEPDPYSPVTHNVSPICE 319
Db 477 ISPIHLDSLRPPVREISITGLTGSTTTTLRTT-----WSPGRSTTPSVSGR 530
QY 320 IQPLSQPSAPIASSPAIDPQSETISSPMPQTHVSGTPPVKASFSS----- 368
Db 531 RNRSTSTP-----SPAELVNDI-----THVPASQIIPALEESCEAVEAREIMW 576
QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSIDLENQVLMKEKALS 410
Db 577 FKTRQGMQKQPCPAGTIGVSTYLCAPDGIWDQPGDLSNCS--SPWVNHITQKLKS-- 632
QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440
Db 633 -GETAANIARELAEOQRHNLNAGDITYSVRAMDQVGLDVLQRLNTPCGKDSAAKSLNK 691
QY 441 -----AQRLLKVVDDIGLQNFN-----TTISLTPSLALAVIR-----VNAS 479
Db 692 LQKRERSRAYVQAMVETVNL-LQPOLNARDLTSDQLRAATMLLDTVEESAFVLAD 750
QY 480 SFNTTTFVAQDPANLQVSLQAPENSIGTITLPSL-----MNNLPADHMLASR 530
Db 751 NLLKTDIVRENTDNIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKONGRNGEIR 810
QY 531 VQNFET--PALFQDPSLENLSL-----ISYVSSSVANLTVRN-----LTR 571
Db 811 VAFVLYNNLGPYL-----STENASKMLGTEAMSTNHSIVNSPVITAANKFESKVLAD 866
QY 572 NVTYTLKHINPSQDELTVRCVFDLGRNGRGWSDNGSGVDRDLRNETICTSHLTSFG 631
Db 867 PVVTVKHQKQSEENFNCSFWSYKRTMTGYSTQGCGRLLTNTKTHTCSCNHLTNFA 926
QY 632 VLL---DLRSTSVLPQAMMALTFITYIGGLSSIFLSVTLVTVIAFEKIRRDYPSKILIQ 688
Db 927 VLMAHVEKHSDAV--HDLLEDVITWVGILLSLVCLLICIFTCFGRGLQSD--RNTHKN 983
QY 689 LCAALLNLNLVFL-----DSWIALYKMOGLCISVAVFLHYFLVLSFTWMGLEAFHMYLA 743
Db 984 LCISLFAELLFLGINRTDQIA-----CAVFAALLHFFFLAAFTWMFLEGVQLYIM 1036
QY 744 LVKVFNT--YIRKYILKFCIVGWGPVAVVVVITLITSPDNYGLSGKFGPSPDFECWI 801
Db 1037 LVEFSESHSRKY---FVLGYGMPALIVAVSAADYRSYG-----TDKVCWL 1082
QY 802 NNAVFYITVGVFCVIFLLNYSMEFIVLVQLCRICK--KKOLGAQRKTSIQDLRSIAGL 859

Db 1083 RLDYFIWISFIGPATLIIMLVNFIAGIALYKMFHTAILKPSGCLDNKISWVIGAIA-L 1141
QY 860 TFLGLGTWGAFAFWGVNVTFMYLFAINTLQGGFIEFYCVAKENVRKOWRRLV---C 916
Db 1142 LCLGLTWAFLYINESTVIMAYLTFISLQGMFIFHCVLQKKVKEYGKCLRTHC 1201
QY 917 C-----GKURLAENSWSKATNGLAKKQTVNOGVSSSSNSLQSSS 956
Db 1202 CSGRSTESSICSGKTSRTPGRVSTGSRIRRMWMDTVRKQSESSFTIGDINSSASLN 1261
QY 957 NSTNSTLLVNDSCSVHASN 977
Db 1262 RGAMANHLISNALLRPHGTNN 1282
RESULT 9
Ti18382
latrophilin-2 (splice variant bbaaf) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18382
R:Matsushita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with different
A:Reference number: Z18869; MUID:99148828
A:Accession: T18382
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1450 <MAT>
A:Cross-references: EMBL:AF111078; NID:94164038; PID:94164039; PIDN:AA05314.1
C:Superfamily: alpha-latrototoxin receptor, calcium-independent
C:Keywords: alternative splicing; G protein-coupled receptor

Query Match 10.0%; Score 534; DB 2; Length 1450;
Best Local Similarity 23.3%; Pred. No. 6.5e-23;
Matches 260; Conservative 168; Mismatches 455; Indels 234; Gaps 48;

QY 90 VETTSND-----VTLSSLPSN-----ETEKTIITIVKTFNAGVKPQR 128
Db 188 IEYASLEDFQNSRQTTTKVKNRVGDTGVVYDGAFFNKRKTR-NIVKYDLTRIKSGE 246
QY 129 NICNLSSICNDUSAFRG---ETMFQYDKES---TVQNOHITNGTLTGVLSSLSEKRS 180
Db 247 AIINYANTHDTSPYRWGKTDIDLAVDENGWLVIYATEQN-----NGMIVLSQNPY 298
QY 181 ELNKTQTLSTETFTMCATAEAQSTLNCFTTKL-----NNTMNACAAIALERVKIRPME 236
Db 299 TLR--FEATWETVDKRAASNAFMICGVLYVRSVYQDNESGTCKNAIDYIYNRLNRGE 356
QY 237 HCCSVRIPCSPSSPEELGKLCQDLPVCLADH-----PRGPP-----FS 277
Db 357 Y---VDVFPFQYQYIAAVDYNPRDNQLYVNNNFILRYSLEFGPPDPAQVPTAVTIT 412
QY 278 SSQSI---PVVPRATVLSQVPKATSPA-----EPPDYSPVTHNVSPICEIQLPS 324
Db 413 SSAEMFKTVTSITTSOKGPMSTTVAGSQEGSKGTAPPAVS--TTKIP--PVTNIEPL- 468
QY 325 POPSAPIASSPAIDMP-----POSE---TSSPMQTHVSGTPPVKASFSPPTVAPANV 377
Db 469 -----PERFCEALDARGIRWPOTQRGMVVERPCPK-----GT-----RGTASYLCVL 510
QY 378 NTTSPAPPVQTDIVNTSS--ISDLENQVLMKEKALSIG-----SLEPNLAGEMINQVSR 429
Db 511 STGTWNPKGPDLSNCTSHVWVNLQAQKIRSGENASLANELAKHTKGPVAGDVSSV-RL 569
QY 430 LHSPPDML-APLAQRLLKVVDDIGLQIN--FSNTTISLTSPLSALAVIRVNAS--SFNTTT 485
Db 570 MEQLVDILDAQLQELKPKSEKDSAGRSYKNAIVDITVDNLLRPEALESWKHMNSSEQAHTAT 629
QY 486 -----FVAQDPANL---QVSLQETQ-----APENSIGTITLPSLMLN---- 518
Db 630 MLDDTLEGAFLAD--NLVEPTRVSMPTENIVLEAVLSTEGVQDQKFFPLGKIGAGSS 687

A:Reference number: Z18869; MUID:99148828		Query Match		10.08; Score 533.5; DB 2; Length 1240;	
A:Accession: T18393		Best Local Similarity		24.24; Pred. No. 5.6e-23;	
A>Status: Preliminary; translated from GB/EMBL/DBJ		Matches		209; Conservative 123; Mismatches 23; Indels 187; Gaps 31;	
A:Molecule type: mRNA					
A:Residues: 1-1240 <MAT>					
A:Cross-references: EMBL:AF111089; NID:g4164060; PID:g4164061; PIDN:AAD05325.1					
C:Superfamily: alpha-latotoxin receptor, calcium-independent					
C:Keywords: alternative splicing; G protein-coupled receptor					
QY	260	LQDPIVCLADHPRGPPFSSQSIPVPRATVLSQVPRKATSAEPDPDYSPTVHNVPSPICE	319		
DB	409	ISPIHLSDLERPPVREISTTGPLGTSTTTTLRTTT	462		
QY	320	IQPLSPQSPAPIASSPAIDMPQSETISSPMQTHVSGTPPPVKASFSS	368		
DB	463	RNRSTSTP	508		
QY	369	-----PTVSAPANVT--TSAP-----PVQTDIVNTSSIDLENQVLMQEKALS	410		
DB	509	FKTRQGMAKQPCPAGTIGVSTYICLAPDGIWDQGPDLNCS--SPWVNHITQKLKS--	564		
QY	411	LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL-----	440		
DB	565	-GETAANIARELAQETRNHLNAGDITYSVRAMDQVLGLDVLQRLNLTGPKGKDSAARSLNK	623		
QY	441	-----AORLLKVVDIGLQNFN-----TTISLTSPSLALAVIR-----VNAS	479		
DB	624	LQKRSRCRAYQAMVETVNNL-LQPALNAWRDLTSDQLRAATMLLDTVEESAFVLAD	682		
QY	480	SENTTFVAQDPANLQVSLQETQAPENSIGTITLPSL-----MNNLPAHDMELASR	530		
DB	683	NLLKTDIVRENTDNIQLEVARLSTEGNLEDLKFPEPTGHGSTIQLSANTLKQNGRGEIR	742		
QY	531	VOFNFFET--PALFQDPSLENLSL-----ISYVISSVANLTVRN-----LTR	571		
DB	743	VAFVLYNNLGPYL-----STENASMKLGTAMSTNHSVINSPVITAAINKEFSNKVYLAD	798		
QY	572	NVTVTLKHNPSODELTVRVCFWDLGRNGRGSGDNGSVKDRRLNETICTCSHLTSFG	631		
DB	799	PVFTVKHKKQSEENFNPCSEFWSYKRTMTGYWSTQGCRLTTNKTHTTSCNHLTNFA	858		
QY	632	VLL---DLSRTSVLPQAOMMALFTITYIGCGLSIFLSVTLVTYIAFEKIRRDYPSKILIQ	688		
DB	859	VLMAHVEVKHSDAV--HDLLLDVITWVGILLSVCLLICIFTFCFFRGLQSD--RNTIHK	915		
QY	689	LCAALLLNLFLL-----DSWIALYKMQGLCISAVFLHYFLVSVFTWGLFAFHMYLA	743		
DB	916	LCISLFAELFLGINTDQPIA-----CAVFAALLHFFLAFTWMLFEGVQLYIM	968		
QY	744	LKVKFNT--YIRKYILKFCIVGWGPAVVVITLITSPDNVGLGSGYKFPNGSPDDFCWI	801		
DB	969	LVEVFESEHSRKY---FYLVGYGMPALIVAVSAADVRSYG-----TDKVCWL	1014		
QY	802	NNNAVFTYVVGFCVIFLLNVSMFIVLVOLCRICK--KKQLGAQRKTSIQDLRSIAGL	854		
DB	1015	RLDTYFIWFSFGPATLIIMLVIFGLIYALYKMFHHTAILKPESGCLDNINTEENRPFKS	1074		
QY	855	---SIAGLTFLLGWTGFAFFAWGPNVTFMYLFAIFNTLQGGFFIFCYCVAKENVRKOW	911		
DB	1075	WVIGATALLCLGLTWAFGLMYINESTVIMAYLFTIENSLQGMFIFHCVLQKKVKEY	1134		
QY	912	RRYL---CCGKLRLAENSWSKATNGLKKQTVNOGVSSSSNSLOSSNSTNTSLTVNN	968		
DB	1135	GKCLRTHCCSG-RSTESSIGSGKTSGRTPGRYSTGSGSRIRRMNDTVRKQSESSFITG	1193		
QY	969	DCSVIASNGNASTERN-GVSFSV	991		
DB	1194	DINSSASLNAREPYRMTSMGVKLN	1217		

Best Local Similarity 23.9%; Pred. No. 7.2e-23;		Matches 206; Conservative 124; Mismatches 333; Indels 198; Gaps 30;	
QY	260	LQDPIVCLADHPRGPPFSSQSIPVPRATVLSQVPRKATSAEPDPDYSPTVHNVPSPICE	319
DB	477	ISPIHLSDLERPPVREISTTGPLGTSTTTTLRTTT	530
QY	320	IQPLSPQSPAPIASSPAIDMPQSETISSPMQTHVSGTPPPVKASFSS	368
DB	531	RNRSTSTP	576
QY	369	-----PTVSAPANVT--TSAP-----PVQTDIVNTSSIDLENQVLMQEKALS	410
DB	577	FKTRQGMAKQPCPAGTIGVSTYICLAPDGIWDQGPDLNCS--SPWVNHITQKLKS--	632
QY	411	LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL-----	440
DB	633	-GETAANIARELAQETRNHLNAGDITYSVRAMDQVLGLDVLQRLNLTGPKGKDSAARSLNK	691
QY	441	-----AORLLKVVDIGLQNFN-----TTISLTSPSLALAVIR-----VNAS	479
DB	692	LQKRSRCRAYQAMVETVNNL-LQPALNAWRDLTSDQLRAATMLLDTVEESAFVLAD	750
QY	480	SENTTFVAQDPANLQVSLQETQAPENSIGTITLPSL-----MNNLPAHDMELASR	530
DB	751	NLLKTDIVRENTDNIQLEVARLSTEGNLEDLKFPEPTGHGSTIQLSANTLKQNGRGEIR	810
QY	531	VOFNFFET--PALFQDPSLENLSL-----ISYVISSVANLTVRN-----LTR	571
DB	811	VAFVLYNNLGPYL-----STENASMKLGTAMSTNHSVINSPVITAAINKEFSNKVYLAD	866
QY	572	NVTVTLKHNPSODELTVRVCFWDLGRNGRGSGDNGSVKDRRLNETICTCSHLTSFG	631
DB	867	PVFTVKHKKQSEENFNPCSEFWSYKRTMTGYWSTQGCRLTTNKTHTTSCNHLTNFA	926
QY	632	VLL---DLSRTSVLPQAOMMALFTITYIGCGLSIFLSVTLVTYIAFEKIRRDYPSKILIQ	688
DB	927	VLMAHVEVKHSDAV--HDLLLDVITWVGILLSVCLLICIFTFCFFRGLQSD--RNTIHK	983
QY	689	LCAALLLNLFLL-----DSWIALYKMQGLCISAVFLHYFLVSVFTWGLFAFHMYLA	743
DB	984	LCISLFAELFLGINTDQPIA-----CAVFAALLHFFLAFTWMLFEGVQLYIM	1036
QY	744	LKVKFNT--YIRKYILKFCIVGWGPAVVVITLITSPDNVGLGSGYKFPNGSPDDFCWI	801
DB	1037	LVEVFESEHSRKY---FYLVGYGMPALIVAVSAADVRSYG-----TDKVCWL	1082
QY	802	NNNAVFTYVVGFCVIFLLNVSMFIVLVOLCRICK--KKQLGAQRKTSIQDLRSIAGL	859
DB	1083	RLDTYFIWFSFGPATLIIMLVIFGLIYALYKMFHHTAILKPESGCLDNKTSVWVIGAL-L	1141
QY	860	TFLGWTGFAFFAWGPNVTFMYLFAIFNTLQGGFFIFCYCVAKENVRKOWRRYL---C	916
DB	1142	LCLLGLTWAFGLMYINESTVIMAYLFTIENSLQGMFIFHCVLQKKVKEYGKCLRTHC	1201
QY	917	C-----GKCLAENSWSKATNGLKKQTVNOGVSSSSNSLOSS	956
DB	1202	CSGRSTESSIGSGKTSGRTPGRYSTGSGSRIRRMNDTVRKQSESSFITGIDINSSASLN	1261
QY	957	NSTNSTLLVNDCSVHASGN	977
DB	1262	RGAMANHLISNALLRPHGTNN	1282

RESULT 12

T18393

latrophilin-3, splice variant abbg, brain-specific - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T18393

R:Matsumita, H.; Leliana, V.G.; Ushkaryov, Y.A.

FEBS Lett. 443, 348-352, 1999

A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with diff

100

Db 918 SLFVAELLFLIGINRTDPIA-----CAVFAALLHFFFLAAFTWMELEGVQLYIMLVE 970
Qy 747 VFNT--YIRKYLKFCIVGVPVAVVTIITISPDNYGLSGYKFPNGSPDDFCWINNN 804
Db 971 VFSEHSRRKY---FYLVGGMPLIIVAVSAADYRSYG-----TDKVCWLRD 1016
Qy 805 AVFYITVGVFCVIFLLNVSMFIVVLVQLCRIKK--KKOLGAQRKTSIQDLRSIAGLTFL 862
Db 1017 TYFWISFIGPATLIIMLVNIFLGIYALYKMFHHTAILKPESGCLDNKISWVIGAI--LLCL 1075
Qy 863 LGITWGAFFAWGPNVTFMYLFAFNTLQGFIFFYCVAKENVRKQW----RRYLCCG 918
Db 1076 LGLTWAFLMYINESTVIMAYLFTFNSLOGMFIFHCVLQKVRKEYGKCLRTHCCSG 1135
Qy 919 KL-----RLAENSND-----WSKTATNGLKQTVNQGVSNNSSLOSS 955
Db 1136 KSTESSIGSGKTSRTPGRVSTGOSRIRRWNDT---VRKQSESSFITGDINSSASL 1191
Qy 956 SNSTNSTTLVNNDCSVHASGN 977
Db 1192 NRGTMANHLMSNALLRPHGTNN 1213
RESULT 15
T17200
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T17200
R:Sugita, S.; Ichchenko, K.; Khvotchev, M.; Sudhof, T.C.
submitted to the EMBL Data Library, July 1998
A:Description: CL family.
A:Reference number: Z18712
A:Accession: T17200
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1341 <SUG>
A:Cross-references: EMBL:AF081159; NID:g3695144; PID:g3695145; PIDN:AAC62665.1
C:Superfamily: alpha-latotoxin receptor, calcium-independent
Query Match 9.9%; Score 532; DB 2; Length 1341;
Best Local Similarity 24.1%; Pred. No. 7.6e-23;
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;
Qy 248 SSPBELGLQCDLQDPVIVCLADHPRGPPSSSQSIPVVPVPRATVLSQVPKATSAEPDPYS 307
Db 466 GSPVHHGQVSY-ISPPHLDSDLRPPVVRGISTGPLGMGTTTTLRTTWNLGRSTT 524
Qy 308 PV-----THNVPSPGIEIQLSPQSPAPIASSPAIDMPQSETISSPMPQTHVSGTTP 360
Db 525 PSLPGRNRSTSTSP--AIEVLDTVTHLPSAASQIPAMEESCEAVEAREIMFKTRQGO 582
Qy 361 PVKASFSPTVS-----APANVNTTSAPPVOTDIVNTSSIDLENQVLQMEKALSIGS 413
Db 593 VAKQSCPAGTIGVYLCIAPDGIWDPQ--DLSNCS--SPWNHITQKLKS--GE 633
Qy 414 LEPNLAGEMINOVSRLLHS-----PDMLAPL----- 440
Db 634 TAANTARELAETNRHNLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAAKSLNKLQK 693
Qy 441 -----AORLLKVDDIGIQLNFSN-----TTISLTSPLALAVIR-----VNASSFN 482
Db 694 RERSCRAYVQAMVETVNNL-LQPQALNWRDLTTSQDLRAATMLLDIVERSAFVLADNLL 752
Qy 483 TTTTFAQDPANLQVSLQAPENSIGTITLPSL-----MNNLPAMDMLASRVQF 533
Db 753 KTDIVRENTDNIQLEVARLSTEGNLEDKLPENTGHGTSIQLSANTLKQNGRNGEIRVAF 812
Qy 534 NFET--PALFOQPSLENLSL-----ISVYSSSVANLTVRN-----LTRNVT 574
Db 813 VLYNLGPYL-----STENASMKLGTTEAMSTNHSVIVNPSVITAANKFESKNKVLADPV 868

Qy 575 VTLKHINPSODELIVRCVFDLGRNGRGSGSDNCGSKVDRLNETICTCSHLTSEGVLL 634
Db 869 FTVKHIKQSEENFNPCSWFSYSKRTMTGYWSTQGRLLTTNKTTCSCNHLTNEAVLM 928
Qy 635 ---DLSTRSVLPQAOMALTEITYIGCGSSIFLSVTLVYIAFEKIRRDYPPSKILQLCA 691
Db 929 AHVEVKHSDAV--HDLLDVITWVIGILLSVCLLCIFCFEFGLOSD--RNTIHRNLCI 985
Qy 692 ALLLINLVFL-----DSWIALYKMOGLCISVAVLHYFLVLSFTWGLAEAFMYIALVK 746
Db 986 SLFVAELLFLIGINRTDPIA-----CAVFAALLHFFFLAAFTWMELEGVQLYIMLVE 1038
Qy 747 VFNT--YIRKYLKFCIVGVPVAVVTIITISPDNYGLSGYKFPNGSPDDFCWINNN 804
Db 1039 VFSEHSRRKY---FYLVGGMPLIIVAVSAADYRSYG-----TDKVCWLRD 1084
Qy 805 AVFYITVGVFCVIFLLNVSMFIVVLVQLCRIKK--KKOLGAQRKTSIQDLRSIAGLTFL 862
Db 1085 TYFWISFIGPATLIIMLVNIFLGIYALYKMFHHTAILKPESGCLDNKISWVIGAI--LLCL 1143
Qy 863 LGITWGAFFAWGPNVTFMYLFAFNTLQGFIFFYCVAKENVRKQW----RRYLCCG 918
Db 1144 LGLTWAFLMYINESTVIMAYLFTFNSLOGMFIFHCVLQKVRKEYGKCLRTHCCSG 1203
Qy 919 KL-----RLAENSND-----WSKTATNGLKQTVNQGVSNNSSLOSS 955
Db 1204 KSTESSIGSGKTSRTPGRVSTGOSRIRRWNDT---VRKQSESSFITGDINSSASL 1259
Qy 956 SNSTNSTTLVNNDCSVHASGN 977
Db 1260 NRGTMANHLMSNALLRPHGTNN 1281
RESULT 16
T18381
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18381
R:Matsushita, H.; Lellanova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with di
A:Reference number: Z18869; MUID:99148828
A:Accession: T18381
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1407 <MAT>
A:Cross-references: EMBL:AF111077; NID:g4164036; PID:g4164037; PIDN:AAD05313.1
C:Superfamily: alpha-latotoxin receptor, calcium-independent
C:Keywords: alternative splicing; G protein-coupled receptor
Query Match 9.9%; Score 531.5; DB 2; Length 1407;
Best Local Similarity 24.2%; Pred. No. 8.7e-23;
Matches 258; Conservative 161; Mismatches 422; Indels 225; Gaps 48;
Qy 90 VETTSLND-----VTLSLPSN-----ETEKTITIVKTFNAGSVKQK 128
Db 188 IEVASLEDQNSRQTITYKLPNVRVDGTFVYDCAVFENKERTR-NIVYDLRTRIKSGE 246
Qy 129 NTCNLSSICNDASAFFRG---EIMPOYDKES-----TVPQNHITNGTLTGLVLSLSEKRS 180
Db 247 AITNANYHDTSPYRWGGKTDIDLAVDENGLWVIYATEQN-----NGMIVISOLNDPY 298
Qy 181 ELNKTLOTSETYFIMCATAEAQSTLACTFTIKL-----NNTMNACAAIAALERVIRKPE 236
Db 299 TLR--FEATWETVYDKRAASNAFMICGVLYVRSVYQDNSESTCKNAIDYIYNTRLNRCGE 356
Qy 237 HCCCSVRIPCSPSEELGKLCQDLPVCLADH-----PRGPP-----FS 277
Db 357 Y-----VDVPPNQYQYIAADVNDPRDNLQYVWNNNFILRYSLEFGPPDPAQVPTTAVTIT 412
Qy 278 SSOSI---PVVPVPRATVLSQVPKATSA-----EPPDYSPVTHNVPSPGIEIQLPS 324

Db 413 SSAEMFKTTVTSTTSQKPMSTTVAGSQEGSKGTAPPVAVS--TTKIP-PVTNIFPL- 468
 QY 325 PQSPAPIASSPAIDMP---POSE---TTSPPMQTHVSGTPPPVKASFSPSTVSAPANV 377
 Db 469 -----PERFEALDARGIRWPTQGMVVERPCPK-----GT-----RGTASYLCVL 510
 QY 378 NTTAPPVQTDIVNTSS---ISDLENQVLOMEKALSIG-----SLEPNLAGEMINOVSR 429
 Db 511 STGTWNPKGPDLSNCTSHWNQLAQKIRSGENASLANELAKHTKGPVAGDVSSV-RL 569
 QY 430 LHSPPDML-APLAQRLKVVDDIGQLN--FSNNTTSLTSPSLALAVIRNAS--SFNTTT 485
 Db 570 MEQLVDIILDAQLOELKPSKDSAGRSYKALVDTVDNLLRPEALESKHMNSSEQAHTAT 629
 QY 486 -----FVAQDPANL-----QVSLTEQ-----APENSIGITILPSSLMN----- 518
 Db 630 MLDDTLBERGAFVLAD--NLVETRVSMPTENIVLEAVLSTEGQVQDFKPLGKAGASS 687
 QY 519 -NLPAHDMELASR---VQNFETFPALFQDPSLEN-----LSLSIYVISS 559
 Db 688 IQLSANTVKQNSRNGLAKLVFIYRSLGQFLSTENATIKLGADFIGRNSITAVNSHVISV 747
 QY 560 SVANLTVR-NLIRNVTVLKHNPSODELTVCVFDLGRNGRGSGDNGCSVKDRRLN 618
 Db 748 SINKESSRVYLTDPVLFPLHIDP-DNYFNANC SFWNSYERTMMGYSTOGCKLVDTNKT 806
 QY 619 ETICTSHLTSGVLLDLSRTSVLP-AQMMALTFITYIGGLSSIFLSVLTVTYIAFEKI 677
 Db 807 RTTCACSHLTNFAILMAHREIAYKGVHLLLTIVTWGIVISLVLCUACIFTCFFRGL 866
 QY 678 RRDYPSKILIOALALLNLVFLDSWTALYKMOGLCISVAVFLHYFLVLSFTWMGLEA 737
 Db 867 QSD-RNTIHKNLCLNLFIAEFLIG--IDTKYMIACPIFAGLLHFEFLAAFAAMWCL 923
 QY 738 FMYLALVKVENT-YIRKYLKFCIVGVPVAVVVTIILTISPNDYGLSGYKFPNGSPD 796
 Db 924 VLYLMLVEFESEYSRKY--YYVAGYLFPAVVGVSAAIDYKSYG-----TE 970
 QY 797 DFCWNNNAVYITVGVFCVIFLLNVSMFIVVLVOLCRICKKKQKLGAKRTSIQDLRS- 855
 Db 971 KACWLHVDNFIWFGPVTFIILLNI--IFLVIPLKMWKHSNTLKPDSRLLENKSW 1027
 QY 856 IAG---LFTLLGITWGAFAFPWPVNTFMYLFAFNTTQGFIFIPYCVAKENVRKOW- 911
 Db 1028 VLGAFAALLCLGLTWSFGLFNEETIIVMAYLFTFNFAPQGVFIHFALQKVRREY 1087
 QY 912 ---RRLCCGKL-----RLAENSWSKATNGLKKTQVNOGVSSSSNSLQ 953
 Db 1088 KCFRHSYCCGGLPTESPSSHYKASTRTSARYSSGTQSRIRRMWNTVTKQSSSFISGD 1147
 QY 954 SSSNSTNTLLVNNDCSVHAG-----NGNASTERNGVSFSVQNGD 995
 Db 1148 INSTSTLNOGHSNLNARDTSAMDITPLNGNFNN-----SYSLRKGD 1188
 RESULT 17
 T14327
 alpha-latrototoxin receptor 3, calcium-independent - rat
 N:Alternate names: G-protein coupled receptor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
 C:Accession: T14327
 R:Ichchenko, K.A.; Bittner, M.A.; Krasnoperov, V.; Little, A.R.; Chepurny, O.; Holz, R.
 J. Biol. Chem. 274, 5491-5498, 1999
 A:Title: A novel ubiquitously expressed alpha-latrototoxin receptor is a member of the CIP
 A:Reference number: Z17983; MUID:99150330
 A:Accession: T14327
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1350 <ICH>
 A:Cross-References: EMBL:AF063103; NID:G3882980; PID:G3882981; PIDN:AAC77816.1
 C:Genetics:

A:Gene: C1RL-3
 C:Superfamily: alpha-latrototoxin receptor, calcium-independent

Query Match 9.9%; Score 531.5; DB 2; Length 1550;
 Best Local Similarity 24.0%; Pred. No. 9.9e-23;
 Matches 216; Conservative 135; Mismatches 347; Indels 203; Gaps 35;

QY 248 SSPEELGKQCDLQDPITVCLADHPRPFPSSSSQSPVVRATVLSQVPKATSFABEPPDYS 307
 Db 466 SGPVHHGVSY-ISPPIHLDSDLERPPVRGISTGTPLGMSGSTTTTLRTTTNLSGRST 524
 QY 308 PV-----THNVSPIGEIOPLSPQSPAPIASSPAIDMPQSETISSPMPQTHVSGPPP 360
 Db 525 PSLGRRNRSTSPSP--AIEVLVDVTHLPSAASQIPAMEESCEAVEAREIMWFTRQOG 582
 QY 361 PVKASFSPSTVS-----APANVNTTSAPPVQTDIVNTSISDLENQVLOMEKALSIGS 413
 Db 583 VAKQSCPAGTIGVSTYLCIAPDGIWDPGP-----DLSNCS--SPVNHITOKLKS--GE 633
 QY 414 LEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440
 Db 634 TAANIARELAEQTRNLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAAKSLKQK 693
 QY 441 -----AQRLLKVVDDIGLQNFEN-----TTISLTSPSLALAVIR-----VNASSFN 482
 Db 694 RERSCRAYVOAMVEIVNNL-LQPALNARDLTTSQLRATMLDITVEESAFVLADNLL 752
 QY 483 TTTVAQDPANLQVLETOAPENSIGITITLPSSL-----MNNLPAHDMELASRVQF 533
 Db 753 KTDIVRENTDNIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLQKNGRNGEIRVAF 812
 QY 534 NFEET--PALFQDPSLENL-----ISYVSSSYANLTVRN-----LTRNVT 574
 Db 813 VLYNNLGPYL-----STENAMKLGTEAMSTNHSVIVNTPVITAINKEFSKNVYLADPV 868
 QY 575 VTLKHINPSODELTVCVFDLGRNGRGSGDNGCSVKDRRLNETICTSHLTSGVGLL 634
 Db 869 FTVKHIKQSENEFNPCSFWSYKRTMTGYWSTQGCRLTTNKTHTTSCNHLNFAVL 928
 QY 635 ---DLSRTSVLPQAQMMALTFITYIGGLSIFLSVTLVYIAEKIRRDYPSKILQICA 691
 Db 929 AHVEVKHSDAV--HDLDDVITWVGILLSLVCLLICIFTFCFFRGLQSD-RNTIHKNL 985
 QY 692 ALLLLNLVFL-----DSWIALYKMOGLCISVAVFLHYFLVLSFTWMGLEAFHMYLALVK 746
 Db 986 SLFVAELLFLIGINFTDQPIA-----CAVFAALHFFFLAFTWMLFEGVQYIIMLVE 1038
 QY 747 VENT--YIRKYLKFCIVGVPVAVVVTIILTISPNDYGLSGYKFPNGSPDPCWINNN 804
 Db 1039 VFBEHSRRKY--FYLGVGMPALIVAVSAADVRSYG-----TDKVCWLRLD 1084
 QY 805 AVFVITVGVFCVIFLLNVSMFIVVLVOLCRICK--KKQLGAQRKTSIQDLR----- 854
 Db 1085 TYFWSFIGPATLILMLNIFLGIALYKMFHTAILKPSGCLDNINEDNRPFIKSWI 1144
 QY 855 SIAGLTFLLGITWGAFAFPWPVNTFMYLFAIFNTLQGFIFIFYCVAKENVRKOW--- 911
 Db 1145 GATALLCLGLTWAFGLMYNESTVIMAYLFTIFNSLQMGFIHFVLCVOKKVRKEGKC 1204
 QY 912 -RRLCCGKL-----RLAENS-----WSKATNGLKKTQVNOGVSS 947
 Db 1205 LRTHCCSGKSTESSIGSGKTSGRTPGRYSTGSRIRRMWNT-----VRKQSSSFTG 1260
 QY 948 SSSNLOSSSSNSTNTLL-----LVNN--DCSVHAS--GNGNASTERNGVSFSVQNG 994
 Db 1261 DINSSASLNGSYLPCIQACVTYLEGLLNARDTSVMDTLPLNGN-----HGNSYSIAGG 1315
 QY 995 D 995
 Db 1316 E 1316

[illegible]

QY 744 LKVKENT--YIRKYLKFCIVGWPVAVVVTIITISPDNYGLSGYKFPNGSPDDFCWI 801
 Db 1037 LVEVESESRKY---FYLVGMPALIVAVSAVRSYG-----TKVCWL 1082

QY 802 NNAVYITVVGFCVIFLLNVSMFIVLVOLCRICK--KKOLGAQRKTSIODLRSIAGL 859
 Db 1083 RLDYFIWFSFIGPATLIIMLVFLGIALYKMFHTATLKPDSEGLDNKISWVIGATA-L 1141

QY 860 TFLGITWGAFAFAMGPVNVTFMYLFAINTLOGFFIFICYVAKENYRKQWRVYL--C 916
 Db 1142 LCLGLTWAFGLMYINESTVIMAYLETFINSLQGMFIFPHCVIQQKVKYKGCRLRHC 1201

QY 917 CGKRLAENSDWKTATNGLKKTOTVQGVSSSSSSLOSSNSTSTTLVNNDCSVHAG 976
 Db 1202 CSG-RSTESSIGSGTSGRTPGYTGSGSRIRRMNDTVRKQSESEFICDINSASL 1260

QY 977 NCNASTERN-GVSFSV 991
 Db 1261 NREPYRETSMGVKLNI 1276

RESULT 20
 T18386
 latrophilin-2 (splice variant bbabf) - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T18386
 R:Matsushita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.
 FEBS Lett. 443, 348-352, 1999
 A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with different
 A:Reference number: Z18869; MUID:99148828
 A:Accession: T18386
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1463 <MAT>
 A:Cross-references: EMBL:AF111080; NID:g4164043; PIDN:AAD05316.1
 C:Superfamily: alpha-latrototoxin receptor, calcium-independent
 C:Keywords: alternative splicing; G protein-coupled receptor

Query Match 9.9%; Score 528.5; DB 2; Length 1465;
 Best Local Similarity 22.9%; Pred. No. 1.4e-22;
 Matches 259; Conservative 165; Mismatches 462; Indels 243; Gaps 46;

QY 90 VETSLND-----VTLSLPSN-----ETEKTITIVKTFNAGSVKPKQR 128
 Db 188 IEYASLEDFQNSRQTTVKLPKNVDGTGFVVDGAVFENKERTR-NIVKYDLRTFKSGE 246

QY 129 NICNLSSICNDSAFFRG---ETMFQYDKES-----TVPQNHITNGTLTGVLSELKRS 180
 Db 247 ALIANYAHDTSPYRWGKTDIDLAVDENGWLVYIATEQN-----NGMIVISQLNPY 298

QY 181 ELNKTLOTLSFTYFMCAAEASTLNCFTFKL-----NNTMNACAAALALERVKIRPME 236
 Db 299 TLR--FEATWETVYDKRAASNAFMICGVLYVRSVQVDNESETEGKNAIDYINTRLNKE 356

QY 237 HCCSVRIPCSPSPPEELKGLQDLODPIVCLADH-----PRGPP-----FS 277
 Db 357 Y-----VDVPPFNQYIAADVNDPNQNLVWNNNTILRYSLEEGPDPQAQVPTAVTIT 412

QY 278 SSQSI---PVVPRATVLSQVPKATSA-----EPDDYSPVTHNVFSPGIEQPLS 324
 Db 413 SSAEMFTTSTTSQKGMSTTIVAGSQEGSKGKAPPAVS--TTKIP--PVTNIFPL- 468

QY 325 PQSAPIASSPAIDMP-----POSE---TISSPMQTHVSGTTPPVKASFSPPTVSAPANV 377
 Db 469 -----PREFCALDARGTRWQTRQGMVVERCPK-----GT-----RGTSYLCVL 510

QY 378 NTSAPPVQTDIVNTSS--ISDLNQVLQMEKALSIG-----SLEPNLAGEMINQVSR 429
 Db 511 STGWNFKGPDLSNCTSHWNQLAQKIRSGENASLANELAKTKGPFVAGDVSSSV-RL 569

QY 430 LHSPPDML-APLAQRLLKVDDIGLQLN--PSNTTISLTSPSLALAVIRVNAS-SENTTIT 485
 Db 570 MEQLVDILDAQQLKPKSEKDSAGRSYNKAIVTDVNDLLRPEALESKWHMNSSEQAHTAT 629

QY 486 -----FVAQDPANL-----QVSLETO-----APENSIGTITLPSLNM----- 518
 Db 630 MLLDTEEGAFVLAD--NLVEPTFVSMPTENIVLEAVLSTEGQVDFKFLGKAGSS 687

QY 519 -NLPAHDMELASR---VQPNFFETPALFQDPSLEN-----LSLSIVSS 559
 Db 688 IQLSANTVQKNSRGLAKLFIYIYRSLQGLSTENATIKLGADFTGRNSTIAVNSHVISV 747

QY 560 SVANLTVR-NLNRNTVTTLKHINPSODELTVRCVFDLGRNGRGGSWDSNGSCVDRRLN 618
 Db 748 SINKESSRYLTDPLVLTPLPHIDP-DNYFNANCSEFWNSERTMMGYWSQGGKLVDTNKT 806

QY 619 ETICCSHLTSGVLDDLSTRTSVLP-AQMMALTPITTVIGCLSSIFLSVTLVTVYIAFEKI 677
 Db 807 RTTCACSHLTNFAILLMAHREIAYKDGVHELLTVITVWGVIVISLCLAICTFFCFEGRGL 866

QY 678 RRDYPSKILIQICALLLNVLFLDLSWIALYKMOGLCISVAVFLHYFLVLLVFTWMLGA 737
 Db 867 QSD-RNTTHKNLCINLFIAEFIFLG--IDTKYMIACPIFAGLLHFFFLAAFAWMCLEG 923

QY 738 FMYLALVKVNT-YIRKYLKFCIVGWPVAVVVTIITISPDNYGLSGYKFPNGSPD 796
 Db 924 VOLYLMLVEFSESRKY--YVAGYLPATVVGSAADYKSYG-----TE 970

QY 797 DFCWNNNAVYITVVGFCVIFLLNVSMFIVLVOLCRICKKKKQKLGAKRKTSIODLRSI 856
 Db 971 KACWLHVDNYFIWFSFIGPATLIIMLVFLGIALYKMFHTATLKPDSEGLDNKISWVIGATA-L 1030

QY 857 AG-----LTFLLGITWGAFAFAMGPVNVTFMYLFAINTLOGFFIFIF 900
 Db 1031 DGYNTDLPGSVWLGAFALLCLGLTWSFGLLFNEETIVMAYLFTIFNAFGVFIPIFH 1090

QY 901 CVAKENVRKQW---RRYLCCGKRLAENSDWKTAT-----NGL 936
 Db 1091 CALQKKVRKEYGKCFRHSYCCGGLPTESPSSSVKASTRTTSARYSSGQSRIRRMNDIV 1150

QY 937 KKQIVNQGVSSSSNSLQSSNSTSTTLVNNDCSVHAGSNGNASTERNGVSVFVQNGDV 996
 Db 1151 RKQSESSFIGSDINSTSTLNQGMGTNYLTLNPLLRPHGTNNPYNTLLAETVVCNAPSAPV 1210

QY 997 CLHDFTQKOHMFNEKEDSC-----NGKGRMALRRTSKRGSILHETE 1036
 Db 1211 ----FNSPGHSLNNARDTSAMDTPPLNGPNNSYSLRKGNDYNSVQVVD 1255

RESULT 21
 T18386
 latrophilin-2 (splice variant bbabf) - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T18386
 R:Matsushita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.
 FEBS Lett. 443, 348-352, 1999
 A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with di
 A:Reference number: Z18869; MUID:99148828
 A:Accession: T18386
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1463 <MAT>
 A:Cross-references: EMBL:AF111082; NID:g4164046; PID:g4164047; PIDN:AAD05318.1
 C:Superfamily: alpha-latrototoxin receptor, calcium-independent
 C:Keywords: alternative splicing; G protein-coupled receptor

Query Match 9.9%; Score 527.5; DB 2; Length 1463;
 Best Local Similarity 23.0%; Pred. No. 1.6e-22;
 Matches 260; Conservative 168; Mismatches 455; Indels 247; Gaps 48;

QY 90 VETSLND-----VTLSLPSN-----ETEKTITIVKTFNAGSVKPKQR 128

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Db 1208 V-----FNSPGHSLNNARDTSAMDTPLPLNGNFNNNSYSLRKGNDYNDVQVVD 1253

RESULT 22
T18383
latrophilin-2, splice variant bbabe - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18383
R:Matsushita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with di
A:Reference number: Z18869; MUID:99148828
A:Accession: T18383
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1422 <MAY>
A:Cross-references: EMBL:AF111079; NID:g4164040; PID:g4164041; PIDN:AAD05315.1
C:Superfamily: alpha-latrotoxin receptor, calcium-independent
C:Keywords: alternative splicing; G protein-coupled receptor

Query Match 9.8%; Score 526; DB 2; Length 1422;
Best-Local Similarity 23.8%; Pred. No. 1.8e-22;
Matches 257; Conservative 158; Mismatches 429; Indels 234; Gaps 46;

QY 90 VETTSLND-----VTLSLLPSN-----ETEKTKITIVKTFNAGVKPQR 128
Db 188 IEYASLEDFQNSRQTTTYTKLPNRVDGTGFVVDGAVFFNKERTR-NIVKYDLRLTRIKSGE 246
QY 129 NICNLSSICNDSAFFRG---EIMFYDKES-----TVPONQHTNGTLTGVLSELKRS 180
Db 247 AIINYANYHDTSPYRWGGKTDIDLAVDENGWLVIYATEQN-----NGMIVISQNLNY 298
QY 181 ELNKTLOTSETYFIMCATAEQAQSTLNCFTTKL-----NTMNAACAAIALERVKIRPME 236
Db 299 TLR--FEATWETVYDKRAASNAFMICGVLYVRSVQDNESETGKNAIDYIYNLRNGE 356
QY 237 HCCGSVRIPCSPSEELGKLDQDPIVCLADH-----PRGPP-----FS 277
Db 357 Y----VDVPFQYQYIAVDYNDPRDQNLVWNNFILRYSLEFGPPDPAQVPTAVTIT 412
QY 278 SSQSI---PVVPRATVLSQVPKATSA-----EPPDYSPVTHNVPSPIGEIOPLS 324
Db 413 SSAEMFKTTVSTTSQKGMSTTVAGSQSGKTKAPPAVS--TTKIP-PVTNIEPL- 468
QY 325 PQSAPIASSPAIDMP---POSE---TISSPMQTHVSGTTPPVKASFSSPTVSAPANV 377
Db 469 -----PERFCEALDARGIRWPQTRGMVVERPCPK---GT-----RGTASYLCVL 510
QY 378 NTTAPPVQTDIVNTSS---ISDLENQVLOMEKALSIG-----SLEPNLAGEMINQVSR 429
Db 511 STGTWNPKGPDLSNCTSHWVNLQAQKIRSGENAAASLANELAKHTKGFVAGDVSSV-RL 569
QY 430 LHSPPDML-APLAQRLLKVVDIGLQNLN--FSNTTISLTPSLALAVIRYNAS--SENTTT 485
Db 570 MEQLVDILDAQLELKPSEKDSAGRSYNAIVTDVNLRLPEALESWKHNSSQAHAT 629
QY 486 -----FVAQDPANL---QVSLETO-----APENSIGTITLPSLLMN----- 518
Db 630 MLLDLEEGAFVLAD--NLVEPTRVSMPTENIVLEAVLSTEGOVQDFKPLGIKAGSS 687
QY 519 -NLPAHDMELASR---VQNFETFPALFQDPSLEN-----LSLSYVSS 559
Db 688 IQLSANTVQKNSRNLAKLVFIYRSLGQFLSTENATIKLGADFIGRNSTIAVNSHVISV 747
QY 560 SVANLTVR-NLTRNVTVTLKHINPSODELTVRCVFDLGRNGRGWSDNGSCVKDRRLN 618
Db 748 SINKESRVYLDVPLVTLPHIDP-DNYFNANGSFNYSERTWMGYWSTQCKLVDINKT 806
QY 619 ETICFCSHLTSPGVLLDLSRTSVLP-AQMMALFTFYIGGLSIFLSFLVTVYAEPI 677
Db 807 RTTCACSHLTNFAILMAHREIAYKDGVHLLLTVTWVGIVISLVCLAICITFCFFRGL 866
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QY 441 -----AORLLKVVDDIGLQNFN-----TTISTSPSLALAVIR-----VNASSFN 482
 Db 694 RERSCRAYVQAMVETVNNL-LQOALNAWROLTTSDQLRAATMLLDTVEESAFVLADNLL 752
 QY 483 TTTTFVADPANLOVLESTQAPENSIGITITLPSL-----MNNLPAHDMELASRVQF 533
 Db 753 KTDIVRENTNIOLEVARLSTEGNELEDLKFPENTCHGSTIOLASANTLKONGRNGEIRVAF 812
 QY 534 NFFET--PALFQDPSLENLSL-----ISVYISSVANLTVRN-----LTRNVT 574
 Db 813 VLXNNLGPYL-----STENASMKLGTEAMSTNHSVTNVPVITAANKPEKNVYLADPV 868
 QY 575 VTLKHINPSQDELTVRCVFDLGRNGRGSGSDNCVKDRNLNETICTCSHLTSPGVLL 634
 Db 869 FTVKHIOKEENFNPNCSFNSYSKRTMTGYSTQCGRLTTNKTTHCTSCNHLITNFAVLM 928
 QY 635 ---DLRSVLPQAOMMALTFITYIGCGLSIFLSVTLVTYIAFEKIRRDYPSKILLQCA 691
 Db 929 AHVEVKHSDAV--HDLLDVITWVGILLSLVCLLICITFCFFERGLQSD-RNTIHKNLCL 985
 QY 692 ALLLLNLVFL-----DSWIALYKMQGICISVAVELHYFLVSTWGLEAFHMYLALVK 746
 Db 986 SLFVAELLFLIGINRTDPIA-----CAVFAALLHFFFLAFTWMELEGVOLYIMLVE 1038
 QY 747 VENT--YIRKYLKFCIVGWGPVAVVVTIILTISPDNYGLSGYKFPNGSPDDFCWINNN 804
 Db 1039 VFSEHSRRKT---FYLGYGMPALIVAVSAANDVRSYG-----TDKVCWLRD 1084
 QY 805 AVEYITVGVFCVIFLLNVSMFIVVLVOLCRICK--KKQLGAQRKTSIODLSRIAGLTL 862
 Db 1085 TYFTWFIGPATLIIMLVIFLGIALYKMFHRTAILKPESGCLDNKSVWIGAIA-LLCL 1143
 QY 863 LGITWGAFFAWGPVNVTFMYLFAFNLTLOGFFIEFYCAKENVRKOW---RRYLCCG 918
 Db 1144 LGLTWAFGLMYNESTVJZMAYLTFINSLQGMFFIFHCVLQKKVKEKGCULRTHCCSG 1203
 QY 919 FLRLAENSWSKATNGLKTKVQNGVSSSSNSLOSSNST---NSTLLVNNDCSVHAS 975
 Db 1204 K---STESSIGSGTSG--SRTPGRYSQSGSRIRRMWNTVRKQSESSFITGINSAS 1258
 QY 976 GNGNASTERN-GVSESV 991
 Db 1259 LNREPYRETSMGVLNI 1275
 RESULT 25
 TI8385
 latrophilin-2 (splice variant bbae) - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 R:Matsumura, H.; Leliana, V.G.; Ushkaryov, Y.A.
 FEBS Lett. 443, 348-352, 1999
 A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with diff
 A:Reference number: Z18869; MUID:99148828
 A:Accession: T18385
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1420 <MAT>
 A:Cross-references: EMBL:AF111081; NID:g4164044; PID:g4164045; PIDN:AAD05317.1
 C:Superfamily: alpha-latrototoxin receptor, calcium-independent
 C:Keywords: alternative splicing; G protein-coupled receptor
 Query Match 9.8%; Score 525; DB 22; Length 1420;
 Best Local Similarity 23.9%; Pred. No. 2.1e-22;
 Matches 258; Conservative 161; Mismatches 422; Indels 238; Gaps 48;
 QY 90 VETSLND-----VTLSLPSN-----EFETKTIIVTKTNASGVKRPQR 128
 Db 188 IEYASLEDFQNSRQTITKPLNRVDGTGFVYDGAFFENKERTR-NIVKYDLRTRIKSGE 246

Search completed: May 23, 2002, 07:39:39
 Job time: 198 sec

QY 129 NICLSSICNDSPFRG---EIMFOYDKES-----TVPQNOHITNGTLGVLSLSELKRS 180
 Db 247 AIINYAVHDTSPIRWGCKTDIDLAVDENGWIVIVATEQN-----NGMIVISOLNPY 298
 QY 181 ELNKTLOTSTYFIMCATAEAQSTLNCFTTKL-----NNTMNACAAIAALERVKRPM 236
 Db 299 TLR--FEATWETVYDKRAASNAFMICGVLYVYRSYQDNSESTGKNAIDYIYNTRLARGE 356
 QY 237 HCCSVIRPSSPELGKLOCDPIVCLADH-----PRGPP-----FS 277
 Db 357 Y-----VDVFFNQVQYIAAVDYNPRDNQLYVNNFNILRYSLFEGPDPAQVTTAVTIT 412
 QY 278 SSQSI---PVVPRATVLSQVPAKATSA-----EPDYSPVTHNVPSPICEIQPLS 324
 Db 413 SSAEMFKTTVTSTTSQKGPMTTIVAGSQEGSKGTAKAPPAVS--TTKID-PVTNIEPL- 468
 QY 325 POPAPATASSAIDMP-----POSE---TISSPMQTHVSGTTPPVKASFSPPSAFANV 377
 Db 469 -----PERFCEALDARGIRWPQOTGRMMVERPCPK-----GT-----RGTAASYLCVL 510
 QY 378 NTSAPPVOTDIVNTSS--ISLENOVLQMEKALSIG-----SLEPNLAGEMINQVSR 429
 Db 511 STGTWNPCKPDLNCTSHWVNOQAQKIRSGENASLANELAKHTKGPVAGDVSSV-RL 569
 QY 430 LHSPPDML-APLAQRLKVVDDIGLQNL-----FSNTTISLSPSLALAV 473
 Db 570 MEQLVDILDAOLOELKPKSEKDSAGRSYNKLOKREKTCRAYLKAIVDTVDNLLRPEALESW 629
 QY 474 IRVNAS-SFNITT-----FVAQDPANL---QVSLQTO-----APENSITG 509
 Db 630 KHMNSSEQAHTMLLDTLEGAFLVAD--NLVEPTRVSMPTENIVLEVAVLSTEGQVOD 687
 QY 510 ITLPSLMN-----NLPAHDMELASR---VQFNFFETPALFQDPSLEN----- 549
 Db 688 FKPLGKIGAGSGIOLASANTVKQNSRGLAKLVILYRSLGQFLSTENATIKLGADFTGR 747
 QY 550 ---LSLSIVYSSSVANLTVR-NLTRNVTVTLKHINPSQDELIVRCVFDLGRNGRGGW 605
 Db 748 NSTIAVNSHVIVSVNKSSESRVYLDVFLTPHIDP-DNYFNANCSFWNSETMMGYW 806
 QY 606 SDNGSVKDRRLNETICTCSHLTSGVLLDLSRTSVLP-AQMMALTFITYIGCGLSIFL 664
 Db 807 STQCGKLVDTNKTRTTCACSHLTNFAILMAHREIAYKGVHCELLTVITWVIVISLVCL 866
 QY 665 SVTLVYTAPEKIRRDYPSKILLQCAALLNLVFLDLSWIALYKMQGLCISVAVFLHY 724
 Db 867 ALCIETFCFFERGLQSD-RNTIHKNLCLINFLIAEFIFLIG--IDTKYMIACPIFAGLLHF 923
 QY 725 FLVSVFTWGLEAFHMYLALVKVENT-YIRKYLKFCIVGWGPVAVVVTIILTISPDNYG 783
 Db 924 FFLAFAFMCLGQVQLYLMLEVEFSEYSRKKY--YVAGYLPFATVVGVSAAIDYKSYG 981
 QY 784 LGSYGKFPNGSPDDFCWINNNNAVFIYTVGVYFCVIFLLNVSMFIVVLQCRICKKKKOLG 843
 Db 982 -----TEKACWLHVDNFIWSFGIPVTFIILLNI---IFLVITLCKMKVKSNTL 1027
 QY 844 AQRKTSIODLRS-IAG---LTFLLGITWGAFFAWGPVNVTFMYLPAFNTLOGFFIFIF 899
 Db 1028 KPDSSRLLENIKSVLWGAFAALLCLLGLTWSFGLLFINETIVMAYLFTIFNAFQGVFIIF 1087
 QY 900 YCAKENVRKOW---RRYLCCCKL-----RLAENSWSKATNGLTKKQOT 940
 Db 1088 HCALOKVKRKEKCPKCRHSYCCGGLPTESPHSSVKASTTRTSARYSSGTQSRIRRMWNT 1147
 QY 941 VNQGVSSSSNSLQSSNSTNTLLVNNDCSVHASG-----NGNASTERNGVSVFVONG 995
 Db 1148 VRKQSESSFISGINDISTSLNQGHSLNNARDTSAMDTPLNNGFN-----SYSLRKG 1201

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2002, 07:37:01 ; Search time 15.11 Seconds
(without alignments)
2659.887 Million cell updates/sec

Title: US-09-731-657-2
Perfect score: 5352
Sequence: 1 SOPEDASGRCAQRFSTLFE.....GRMALRRTSKRGLHFIEQM 1038

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	477.5	8.9	835	1	CD97_HUMAN
2	468.5	8.8	931	1	EMR1_MOUSE
3	438	8.2	886	1	EMR1_HUMAN
4	409	7.6	1572	1	BAI2_HUMAN
5	403	7.5	1522	1	BAI3_HUMAN
6	379.5	7.1	1584	1	BAIL_HUMAN
7	259	4.8	441	1	DIHR_ACHDO
8	235	4.4	496	1	PACR_MOUSE
9	232	4.3	415	1	CRF1_SHEEP
10	231.5	4.3	413	1	CRF2_XENLA
11	230	4.3	415	1	CRF1_RAT
12	228.5	4.3	513	1	PACR_BOVIN
13	227.5	4.3	468	1	PACR_HUMAN
14	225	4.2	415	1	CRF1_MOUSE
15	223.5	4.2	459	1	VIPIR_RAT
16	223.5	4.2	676	1	MTH1_DROME
17	220	4.1	523	1	PACR_RAT
18	219	4.1	395	1	DIHR_MANSE
19	210.5	3.9	444	1	CRF1_HUMAN
20	209.5	3.9	415	1	CRF1_XENLA
21	209	3.9	411	1	CRF2_RAT
22	208	3.9	431	1	CRF2_MOUSE
23	208	3.9	457	1	VIPIR_HUMAN
24	206.5	3.9	445	1	SCRC_RABIT
25	205	3.8	420	1	CRF1_CHICK
26	205	3.8	449	1	SCRC_RAT
27	199.5	3.7	463	1	GLP1_RAT
28	198.5	3.7	464	1	CGRR_RAT
29	197	3.7	411	1	CRF2_HUMAN
30	193	3.6	463	1	GLP1_HUMAN
31	193	3.6	644	1	YQ44_CAEEL
32	192	3.6	478	1	CALR_CAVPO
33	191.5	3.6	489	1	GLP1_MOUSE

34	189	3.5	490	1	CALR_HUMAN
35	188.5	3.5	437	1	VIPIR_MOUSE
36	186.5	3.5	517	1	MTH_DROYA
37	186	3.5	440	1	SCRC_HUMAN
38	186	3.5	550	1	PTR2_HUMAN
39	185	3.5	585	1	PTRR_DIDMA
40	184.5	3.4	461	1	CGRR_HUMAN
41	182	3.4	585	1	PTRR_PIG
42	182	3.4	593	1	PTRR_HUMAN
43	181.5	3.4	1161	1	DAM4_YEAST
44	181	3.4	591	1	PTRR_RAT
45	180.5	3.4	1140	1	YM96_YEAST
46	180	3.4	447	1	VIPIR_CARAU
47	180	3.4	485	1	GLR_RAT
48	179	3.3	458	1	VIPIR_PIG
49	178.5	3.3	516	1	CALR_RAT
50	176	3.3	474	1	CALR_RABIT
51	175.5	3.3	437	1	VIPIR_RAT
52	175.5	3.3	458	1	MTH3_DROME
53	175	3.3	485	1	GLR_MOUSE
54	175	3.3	515	1	CALR_MOUSE
55	174.5	3.3	514	1	MTH_DROME
56	174.5	3.3	591	1	PTRR_MOUSE
57	174	3.3	438	1	VIPIR_HUMAN
58	174	3.3	1533	1	Y586_HUMAN
59	171.5	3.2	468	1	MTH4_DROME
60	171.5	3.2	498	1	CALR_PIG
61	170	3.2	515	1	MTH_DROSI
62	167	3.1	546	1	PTH2_RAT
63	166.5	3.1	637	1	MTHA_DROME
64	166	3.1	1367	1	AMYH_YEAST
65	164	3.1	477	1	GLR_HUMAN
66	164	3.1	1306	1	MSB2_YEAST
67	162	3.0	512	1	MTH2_DROME
68	160.5	3.0	260	1	VIPIR_MELGA
69	160	3.0	553	1	GLP2_HUMAN
70	158.5	3.0	870	1	YCS0_YEAST
71	158	3.0	634	1	HWPI_CANAL
72	155	2.9	5179	1	MUC2_HUMAN
73	154.5	2.9	865	1	CPN_DROME
74	153.5	2.9	462	1	GIPR_MESAU
75	153	2.9	490	1	CAR3_DICDI
76	152.5	2.8	666	1	FZD3_MOUSE
77	151.5	2.8	666	1	FZD3_HUMAN
78	150	2.8	1802	1	HKR1_YEAST
79	149	2.8	550	1	GLP2_RAT
80	149	2.8	921	1	T2D3_DROME
81	148.5	2.8	1794	1	YAV1_SCHPO
82	148	2.8	466	1	GIPR_HUMAN
83	147	2.7	1858	1	P3K2_DICDI
84	147	2.7	2108	1	NOT1_YEAST
85	146.5	2.7	1609	1	FIG2_YEAST
86	146.5	2.7	2004	1	MOZ_HUMAN
87	145.5	2.7	5376	1	ZAN_MOUSE
88	145	2.7	725	1	AGAL_YEAST
89	143	2.7	3149	1	TEGU_EBV
90	143.5	2.7	455	1	GINP_RAT
91	143.5	2.7	673	1	YNM5_YEAST
92	143.5	2.7	1229	1	NI21_HUMAN
93	143	2.7	1163	1	RTN4_RAT
94	143	2.7	1328	1	HUS2_SCHPO
95	142.5	2.7	1849	1	IGA4_HAEIN
96	142.5	2.7	1874	1	POLR_KYVJ
97	142	2.7	475	1	MTHC_DROME
98	141.5	2.6	2194	1	SC16_YEAST
99	141	2.6	522	1	YOW3_CAEEL
100	141	2.6	901	1	Y298_HUMAN

ALIGNMENTS

RESULT 1

CD97	HUMAN	STANDARD;	PRT;	835 AA.
AC	CD97_HUMAN		PRT;	835 AA.
AD	P48960:			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DT	Leucocyte antigen CD97 precursor.			
DE	CD97.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
ON	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=95363161; PubMed=7636245;			
RA	Hamann J., Eichler W., Hamann D., Kerstens H.M.J., Poddighe P.J.,			
RA	Hoovers J.M.N., Hartmann J.M., Strauss M., van Lier R.A.W.;			
RT	"Expression cloning and chromosomal mapping of the leukocyte			
RT	activation antigen CD97, a new seven-span transmembrane molecule of			
RT	the secretin receptor superfamily with an unusual extracellular			
RT	domain.";			
RT	J. Immunol. 155:1942-1950(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Forsklin;			
RA	MEDLINE=96230339; PubMed=8786105;			
RA	Hamann J., Hartmann E., van Lier R.A.W.;			
RT	"Structure of the human CD97 gene: exon shuffling has generated a new			
RT	type of seven-span transmembrane molecule related to the secretin			
RT	receptor superfamily.";			
RT	Genomics 32:144-147(1996).			
RN	[3]			
RP	REVISTONS,			
RA	Hamann J.;			
RP	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: COULD BE A RECEPTOR POTENTIALLY INVOLVED IN BOTH			
CC	ADHESION AND SIGNALING PROCESSES EARLY AFTER LEUKOCYTE ACTIVATION.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: CONTAINS 5 EGF-LIKE DOMAINS.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-1- SIMILARITY: CONTAINS 1 GPS DOMAIN.			
CC	-1- DATABASE: NAME=PROW; NOTE=CD guide CD97 entry;			
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd97.htm".			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X84700; CAA59173.1; .			
DR	EMBL; X94630; CAA64333.1; .			
DR	EMBL; X94631; CAA64333.1; JOINED.			
DR	EMBL; X94632; CAA64333.1; JOINED.			
DR	EMBL; X94633; CAA64333.1; JOINED.			
DR	EMBL; X99830; CAA64333.1; JOINED.			
DR	EMBL; X99831; CAA64333.1; JOINED.			
DR	EMBL; X99832; CAA64333.1; JOINED.			
DR	EMBL; X94634; CAA64333.1; JOINED.			
DR	EMBL; X94635; CAA64333.1; JOINED.			
DR	EMBL; X94636; CAA64333.1; JOINED.			
DR	EMBL; X94637; CAA64333.1; JOINED.			
DR	EMBL; X94638; CAA64333.1; JOINED.			
DR	EMBL; X94639; CAA64333.1; JOINED.			
DR	EMBL; X94640; CAA64333.1; JOINED.			
DR	EMBL; X94641; CAA64333.1; JOINED.			
DR	EMBL; X94642; CAA64333.1; JOINED.			
DR	EMBL; X94643; CAA64333.1; JOINED.			
DR	EMBL; X94644; CAA64333.1; JOINED.			
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DR	EMBL; X94646; CAA64333.1; JOINED.			
DR	EMBL; X94647; CAA64333.1; JOINED.			
DR	EMBL; X94648; CAA64333.1; JOINED.			
DR	EMBL; X94649; CAA64333.1; JOINED.			
DR	EMBL; X94650; CAA64333.1; JOINED.			
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DR	EMBL; X94656; CAA64333.1; JOINED.			
DR	EMBL; X94657; CAA64333.1; JOINED.			
DR	EMBL; X94658; CAA64333.1; JOINED.			
DR	EMBL; X94659; CAA64333.1; JOINED.			
DR	EMBL; X94660; CAA64333.1; JOINED.			
DR	EMBL; X94661; CAA64333.1; JOINED.			
DR	EMBL; X94662; CAA64333.1; JOINED.			
DR	EMBL; X94663; CAA6433			

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Query Match      8.9%  Score 477.5;  DB 1;  Length 835;
Best Local Similarity 22.5%;  Pred. No. 2.9e-18;
Matches 207;  Conservative 133;  Mismatches 306;  Indels 275;  Gaps 39;

QY 158 PNOHITNGTL-----TGVLSLSELKSELNKTLOTLSETYFIMCAT-----E 201
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 31 PONSVCVNATACRCPGFSFSEIITTP-TETCDDINE-----CATPSKVCSCGFSDCWN 84

QY 202 AGSTLNC-----TFITKLNNTMN-----ACAA 223
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 85 TEGSYDCVCSGPEPVSGAKTFKNESENTODVDECOQNPRLCKSYGTCVNTLGSTYTCQC 144

QY 224 IAALERVKIRPMEHC-----CCSVRIKPCSPSP-----EELGKLQCLDQDPVCLADHPRGPP 275
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 145 LPGEKFIPEDP-KVCTDVNCTSGONCHSTHCLNNGVSCRCR-----PGWQP 194

QY 276 FSSQSIPVPRATVLSQVPKATSEAPDPDYSPVTHN-VPSPIGBIQI-PSPQSPAPIAS 333
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 195 IGS---PNGPNNTVCEDVDECSGQHCDSSTVCFNTVGSYSCRCRPGWKPRHGIP--- 248

QY 334 SPAIDMPQSEITSSPMPOTHVGTGTPPVKASFSSPTVSAPANVNTTSAPPVQTDIVNTS 393
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 249 -----NNGKDIVCEDM--TFSTWTTPPG-----VHSQ 273

QY 394 SISLENOVLQMEKALSLSLEPNLAGEMINQVSRLLHSPDDM--LAP-----LAORLIK 446
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 274 TLSRFFQVQDLGRDSKTSSEAVTIO-NVIKLVDELMEAPGDEALAPPVRLHILATQLLS 332

QY 447 VDDIGIQLNFNTTISLSPSLALAVIRVNASFNTTFFVAQDPANLOVSLTQAPENS 506
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 333 NLEDI-----MRILAKSLPKGPETYISPSNTELTMIQ--ERG 368

QY 507 IGTITLPSLMNLPAMDLMELASRVQNFETPALFOOPS-----LENLS 551
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 369 DKNVTMGOS-----SARMKLN-WAVAAGADPGPAVAGILSIQNNTTLLANAS 415

QY 552 L-----ISYVSISSVANLTVRNLTNRVTVTLKHIN----- 581

DB 416 LNLHKKQAELEBEIVESSIRGVQLRSLASVNSIFLSHNTKELNSPILFAFSLHSSDGE 475

QY 582 -----PSQDEL-----TVRCVFDLGRNGRGSGWSDNGCSVKDRRLNETICTSHLTSG 631
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 476 AGROPAPKDVMPGPROELLCFAFKWSDDRG-GHWATEVCQVLGSKNGSTTCCSHLSFT 534

QY 632 VLLDSRTSVLPQAMMALFTITYIGCLSSIFLSVTLVTYIAFEKIRRDYPSKILIQCA 691
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 535 ILM-----AHYDVDEWKLTLITRVGLALSILFCLLCILTLFLLVRPIQGS-RTTHLHLCI 588

QY 692 ALLLNLVFLDLSWIALYKMQG-----LCISVAVFLHYFLVSEFTWGLFAFMYLALVK 746
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 589 CLFVGSITFL-----AGIENEGQVGLRCLRVAGLLHYCFLAFCWMSLEGLEYFLVVR 643

QY 747 VF--NTYIRKYILKFCIVGWGPVAVVVTIILTISPDPNYGLSGYKFPNGSPDDFCWINN 804
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 644 VFQOGLSTRWL---CLIGYGVPLLVIGVSAALYSKYGPRY-----CWLDFE 689

QY 805 AVFITVVGVCYFIFLLNVMFIVVLVQLCR-----IKKKQLGAQRKTSIQDLRSI 856
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 690 QGFLWSELFGPVTFIILCNAVIFVTWVKLTQKFSEINPDMKKLKKARALITATAQL--- 746

QY 857 AGLTFLGITWGEFAFFANGPVNVTWFLPAINTLOGFFIFCYCAKENVKORWRYLC 916
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 747 ----FLGCTWVFLGFIIDRSLVUTYVETILNCLGAFLLYLLHLLNKKVREYRKYAC 802

QY 917 CGKRLAENSWSK--TATNG 935

DB 803 L-----VAGGSKYSEFTSTSG 819

RESULT 2
EMRL_MOUSE
```

```
EMRL_MOUSE STANDARD; PRT; 931 AA.
Q61549;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Cell surface glycoprotein EMRL precursor (EMRL hormone receptor)
(EMRL OR GPF480).
Mus musculus (Mouse).
Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=BALE/C; TISSUE=Peritoneal cavity;
MEDLINE=96132946; PubMed=8550607;
McKnight A.J., Macfarlane A.J., Dri P., Turley L., Willis A.C.,
Gordon S.;
"Molecular cloning of F4/80, a murine macrophage-restricted cell
surface glycoprotein with homology to the G-protein-linked
transmembrane 7 hormone receptor family.";
J. Biol. Chem. 271:486-489(1996).
[2]
SEQUENCE FROM N.A.
MEDLINE=97312684; PubMed=9169125;
Lin H.H., Stubbs L.J., Mucenski M.L.;
"Identification and characterization of a seven transmembrane hormone
receptor using differential display.";
Genomics 41:301-308(1997).
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION WITHIN TISSUES
AND RECEPTOR SIGNALING.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: IN MACROPHAGES; BUT ABSENT FROM THOSE WHICH
ARE LOCALIZED WITHIN T-CELL AREAS OF LYMPH NODES AND SPLEEN.
CC -!- SIMILARITY: CONTAINS 7 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 GPS DOMAIN.
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; X93328; CAA63720.1; -.
EMBL; U66888; AAC53184.1; -.
HSSP; P07204; IFGD.
GCRDB; GCR_1309; -.
MGD; MGI:106912; Emr1.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR000832; GPCR_secretin.
InterPro; IPR000203; PKD_cys_rich.
Pfam; PF00002; 7tm_2; 1.
Pfam; PF00008; EGF; 6.
Pfam; PF01825; GPS; 1.
PRINTS; PR01128; EMRHORMONER.
SMART; SM00179; EGF_CA; 6.
SMART; SM00001; EGF_like; 1.
SMART; SM00303; GPS; 1.
PROSITE; PS00010; ASX_HYDROXYL; 6.
PROSITE; PS01185; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 5.
PROSITE; PS00221; GPS; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
G-protein coupled receptor; Transmembrane; Receptor; Glycoprotein;
EGF-like domain; Repeat; Signal.
POTENTIAL.
1 27
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CC DR EMBL; X81479; CAA57232.1; -
 DR HSP; P35555; 1ENN.
 DR MIM; 600493; -
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR000203; PKD_cys_rich.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF00008; EGF; 5.
 DR Pfam; PF01825; GPS; 1.
 DR PRINTS; PR01128; EMRIHORMONER.
 DR SMART; SM00179; EGF_CA; 5.
 DR SMART; SM00001; EGF_Like; 1.
 DR SMART; SM00303; GPS; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 6.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 5.
 DR PROSITE; PS02221; GPS; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS02263; G_PROTEIN_RECP_F2_4; 1.
 DR G-protein coupled receptor; Transmembrane; Receptor; Glycoprotein;
 KW EGF-like domain; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 886
 FT DOMAIN 18 886
 FT DOMAIN 18 599
 FT TRANSMEM 600 627
 FT DOMAIN 628 634
 FT DOMAIN 635 656
 FT TRANSMEM 657 666
 FT DOMAIN 667 690
 FT TRANSMEM 691 709
 FT DOMAIN 710 731
 FT TRANSMEM 732 747
 FT DOMAIN 748 776
 FT TRANSMEM 777 794
 FT DOMAIN 795 814
 FT TRANSMEM 815 829
 FT DOMAIN 830 852
 FT TRANSMEM 853 886
 FT DOMAIN 31 79
 FT DOMAIN 80 131
 FT DOMAIN 132 171
 FT DOMAIN 172 213
 FT DOMAIN 221 267
 FT DOMAIN 268 316
 FT DOMAIN 317 599
 FT DISULFID 35 47
 FT DISULFID 41 56
 FT DISULFID 58 78
 FT DISULFID 84 97
 FT DISULFID 91 106
 FT DISULFID 108 130
 FT DISULFID 136 148
 FT DISULFID 142 157
 FT DISULFID 159 170
 FT DISULFID 176 188
 FT DISULFID 182 197
 FT DISULFID 199 212
 FT DISULFID 225 235
 FT DISULFID 229 244
 FT DISULFID 246 266
 FT DISULFID 272 285
 FT DISULFID 279 294
 FT DISULFID 296 315
 FT CARBOHYD 94 94
 FT CARBOHYD 99 99
 FT CARBOHYD 127 127
 FT CARBOHYD 167 167
 FT CARBOHYD 189 189
 FT CARBOHYD 194 194

FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 375 375 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 661 661 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 886 AA; 97680 MW; 7456CA36FBG24D99 CRC64;
 Query Match 8.2%; Score 438; DB 1; Length 886;
 Best Local Similarity 20.8%; Pred. No. 3.9e-16;
 Matches 198; Conservative 149; Mismatches 365; Indels 238; Gaps 38;
 QY 64 EDTNSSLSPPPA-----KLSVVS--FAPSSNE-----VETTSLND-VT 99
 Db 79 KDIDECSSQSPQCPGNSSCKNLGRYKSCLDGFSPTGNDWVPKPGKPNFSCDINECUT 138
 QY 100 LSLPLSNTEKTIIVKTFNAGVQPNICNLSSICNDSAFTRGEIMFQYDKESTVPO 159
 Db 139 SRVCPHS-----DCVNSMGVSCSCQGVFISRNSTCEV-----NECADPR 180
 QY 160 --NOHIT-NGTL-----TGVLSLSLSEKRS-----ELNKTTLTLE 191
 Db 181 ACPEHATCNNTVGNYSFCNCPGFESSHGLSCQGLKASCEIDECTEMCPINSTCTNTPG 240
 QY 192 TYFTMCATAEAQSTLNCFTTILKLNNTMNACAAIAERVKIRPMEHC-----CCSVRIPC 246
 Db 241 SYFTCHPGFAPSSGQLNFTD-----QGVCECRDIDECRQDPSTCGPNSIC 285
 QY 247 PSSPEELGKLOCDLQDPVIVCLADHPRGPP-----FSSSOSI-----PVVPRATVLSOVPKA 297
 Db 286 TNA---LGSYSCGC---IVGFPHNPEGSKQDGNFSCQVLFKCKEDVIPDNKKQIQCOEG 339
 QY 298 TSFAEPDPYSPVTHNVPSPGIGIQLPSPQSPAPIASPAIDMPQSETISSPMPQTHVSG 357
 Db 340 TA-----
 QY 358 TTPPVKASFSSPTVSAPANVNNTSAPPVQTDIVNTSSISD--LENQVLOMEKALSLSLE 415
 Db 342 ---VKPAY---VSFCAQIN-----NIFSVLDKVCENKTTVSLKNTTESFV 381
 QY 416 PNLAGEMINOVSRLLHSPDMLAPLAQRLLKVVDDIGLQNFNTTISLTSPLSALAVIR 475
 Db 382 P-----VLKQISMTWKETKEETSSLATVLESVESMTL-ASFVKP SANVT-PAYRAEVL 434
 QY 476 VNASSFNFTTFAQDPANLQVLETOAPENSTGTITPLPSLMNNLPAHDMELASRVQNF 535
 Db 435 IESKVINKEC-----SEENVTLDLVAKGDKMKIGCSTIEES--ESTETTGVAFVSFGMES 488
 QY 536 FETPALFQD-----PSLENLSLSISYVISSVANLTVRNLTNRVTVTLKHINPSODELTV 589
 Db 489 VLNERFQDQAPLTTSEIKLKMNSRVVGGIMTGEKKDGFSDPIITYTLENVQPKQKFERP 548
 QY 590 RCVFWDLGRNGRGWSDNGCSVKDRRLNETICTCSHLTSFGVLLDLSTRTSVLPAQMMAL 649
 Db 549 ICVSWSTDVKGGR--WTSFGCVILEASETYTICSCNOMANLAVIMASGELTM----DFSL 602
 QY 650 TPTYICGGLSSIFLSVTLVYIAFEKIRRDYPSKILLIOLCAALLLNVLFLDSWITALY 709
 Db 603 YIISHVGIIISLVCVLAIATFLCRSI-RNHNTYIHLHLCVOLLAKTLFL-----AGIH 657
 QY 710 KMOGL--CISVAVFLHYFLVFTWGMLEAFHMYLAL--VKVENTYIRKYI--LKFCIVG 763
 Db 658 KTDNKTCCALLIAGFLHYFLACFFWMLVEAVILFLMVRNLKVVNVFSSRNKMLHICAFG 717
 QY 764 WGVPAVVVTIILTISPNDYNGLSGKPGKPNSSPDPCFWINNNNAFFYITVVGVCYFIFLNV 823
 Db 718 YGLPMLVWVVISASVQPGQYGM-----HNCWLNLTETGFIWSFLGPVCTIVIN- 765
 QY 824 SMFIVVLVQLCRKTKKKK---OLGAQRKTSIQDLRSIAGLTFLGLGTWGAFFAWGPVNV 880
 Db 766 SLLLTWTWLIRQLRSLSSVNAEVSITKDTRLTLTKFAQL-FILGCSWVLGIFQIGPVAGY 824

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881 FMYLFAFNTLQGFIFIFYCVAKENVKQWRRYLCCGKRLRAENSDWSK 930
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
825 MAYLFTIINSLOGAFIFLIHCLLNGQVREYKRWI-TGKTPSSQSQTSR 873

RESULT 4
ID BAI2_HUMAN STANDARD; PRT: 1572 AA.
CC O60241;
WT 16-OCT-2001 (Rel. 40, Created)
PT 16-OCT-2001 (Rel. 40, Last sequence update)
OI 01-MAR-2002 (Rel. 41, Last annotation update)
DE Brain-specific angiogenesis inhibitor 2 precursor.
EE BAI2.
NN Homo sapiens (Human).
NS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCBI_TaxID=9606;
NN [1]
PP SEQUENCE FROM N.A.
AC TISSUE=Fetal brain;
GC MEDLINE=98194217; PubMed=9533023;
SV Shiratsuchi T., Nishimori H., Ichise H., Nakamura Y., Tokino T.;
AA "Cloning and characterization of BAI2 and BAI3, novel genes homologous
PT to brain-specific angiogenesis inhibitor 1 (BAI1).";
XT CytoGenet. Cell Genet. 79:103-108(1997)
NL CYTOGENESIS INHIBITION

```

- 1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN BRAIN. ALSO DETECTED IN HEART, THYMUS, SKELETAL MUSCLE, AND DIFFERENT CELL LINES.
- 1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
- 1- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.

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-!- SIMILARITY: CONTAINS 1 GPS DOMAIN
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or send an email to license@isb-sib.ch).
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EMBL; AB005298; BAA25362.1; -.
MIM; 602683; -.
InterPro; IPR000832; GPCR_secretin.
InterPro; IPR000203; PKD_cys_rich.
InterPro; IPR000884; TSPL.
InterPro; IPR001879; hormn_receptor.
Pfam; PF00002; 7tm_2; 1.
Pfam; PF01825; GPS; 1.
Pfam; PF02793; HRM; 1.
Pfam; PF00090; tsp_1; 4.
SMART; SM00303; GPS; 1.
SMART; SM00008; HormR; 1.
SMART; SM00209; TSPL; 4.
PROSITE; PS00221; GPS; 1.
PROSITE; PS00649; G_PROTEIN_RECP_F2_1; FALSE_NEG.
PROSITE; PS00650; G_PROTEIN_RECP_F2_2; FALSE_NEG.
PROSITE; PS00327; G_PROTEIN_RECP_F2_3; 1.
PROSITE; PS00361; G_PROTEIN_RECP_F2_4; 1.
PROSITE; PS50092; TSPL; 4.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
Repeat.
SIGNALL 1 20
CHAIN 21 1572
DOMAIN 21 924
TRANSMEM 925 945
DOMAIN 946 953
TRANSMEM 954 974
DOMAIN 975 982
TRANSMEM 983 1003
DOMAIN 1004 1024
POTENTIAL.
BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2.
EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).

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CC 584 QDELAVRCVFDLGR-NGRGSGSDNGSVKDRRLNETICTCSHLTSGVLLDLRSVTL 642
CC 812 NGTLNFCVCLWDDSKTNSLGTWQCKTAVLTDASHTKCLCDRLSTFAILAAQPREIIM 871
CC 643 PAQ-MMALFTFITYIGCLSLIFSVTLVTVIAFEKIRRDYPSKILQICAAALLNVLVL 701
CC 872 ESSGTPSVTLI--VSGSLCLALITLAVVAALWRYIRSEIILNFCLSIISNILL 929
CC 702 LDSWIALYKMOGLCISVAVFLHYFLVSVFTWGLAEFMYLALV-KVNTYIRKYILKFC 760
CC 930 VGOQTQHNK--SICTTTAFLEHFFELASFCWLVTEAWQSYMAVTKIRTLIRK---REFL 984
CC 761 IVGWGVPAVVV-TIILTISPNDVGLSGYKFPNGSPDFCWINNNAVYIITVGVFCVIF 819
CC 985 CLGWGLPALVAVTSVGFTRTKGYG-----TDHYCWLSEGLGLLYAFVGPAAAVV 1033
CC 820 LNVSMFIVVLVOLCR-----IKKKQLGAGQ-----RKTSIQDLRSIAGLTF- 861
CC 1034 LVNVGILVFNKLVSRDGLDKLKHRAQOMSEPHSGLTCLKCAKCGVSVTTALSATTAS 1093
CC 862 -----LLGITWGFAPFAM-GPVNVTVMYLFALFNTLQGFIFIFYCVAKEN 906
CC 1094 NAMASLWSSCWVPLLAALTWMSAVLAWTKRSILFQILFAVFDLSLQGFVYVMVHCILRE 1153
CC 907 VRKQWRYLCCGKRLAE---NSDWKSTATNGLKK--QTVNOGVSSSSNSL-----Q 953
CC 1154 VQDAFR---C-RLRNCQDPINADSSSPFNHAGIMTDFEKDVDIACRSVLHKDGPGR 1208
CC 954 SSSNSTNTTLLVNDSCSVHAGNGNASTENGVSFVSONGD-----VCLHDTGTQOHM-- 1007
CC 1209 AATITGTLRSILNDD-----BEEKGTNPEGLSYSTLPGNVISKVITIQPTG-LHMPM 1260
CC 1008 -FNEKEDSCNGKGMALRRT 1026
CC 1261 SMNELSNPCLKKENSELRRT 1280
RESULT 6
BAIL_HUMAN STANDARD; PRT; 1584 AA.
AC O14514; 2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Brain-specific angiogenesis inhibitor 1 precursor.
GN BAIL
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=98054121; PubMed=9393972;
RA Nishimori H., Shiratsuchi T., Urano T., Kimura Y., Kiyono K.,
RA Tatsumi K., Yoshida S., Ono M., Kuwano M., Nakamura Y., Tokino T.;
RT "A novel brain-specific p53-target gene, BAIL, containing
RT thrombospondin type 1 repeats inhibits experimental angiogenesis.";
RL Oncogene 15:2145-2150(1997).
RN [2]
RP INTERACTION WITH BAP1.
RX MEDLINE=98321173; PubMed=9647739;
RA Shiratsuchi T., Futamura M., Oda K., Nishimori H., Nakamura Y.,
RA Tokino T.;
RT "Cloning and characterization of BAI-associated protein 1: a PDZ
RT domain-containing protein that interacts with BAIL.";
RL Biochem. Biophys. Res. Commun. 247:597-604(1998).
CC -!- FUNCTION: LIKELY TO BE A POTENT INHIBITOR OF ANGIOGENESIS IN
CC BRAIN AND MAY PLAY A SIGNIFICANT ROLE AS A MEDIATOR OF THE P53
CC SIGNAL IN SUPPRESSION OF GLOBLASTOMA. MAY FUNCTION IN CELL
CC ADHESION AND SIGNAL TRANSDUCTION IN THE BRAIN.
CC -!- SUBUNIT: INTERACTS WITH BAP1.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. LIKELY TO BE
CC CONCENTRATED AT CELL-CELL ADHESION SITES.
CC -!- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN BRAIN. REDUCED OR NO
CC EXPRESSION IS OBSERVED IN SOME GLOBLASTOMA CELL LINES AND CANCER
CC TISSUES.
CC -!- INDUCTION: BY P53.
CC -!- DOMAIN: THE TSP1 REPEATS INHIBIT IN VIVO ANGIOGENESIS IN RAT
CC CORNEA INDUCED BY BFGF.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- SIMILARITY: CONTAINS 5 TSP TYPE-1 DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 GPS DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AB005297; BAA23647.1; -
CC MIM: 602682;
CC InterPro: IPR000832; GPCR_secretin.
CC InterPro: IPR000203; PKD_cys_rich.
CC InterPro: IPR000884; TSP1.
CC InterPro: IPR001879; hormo_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF01825; GPS; 1.
CC Pfam; PF02793; HRM; 1.
CC Pfam; PF00090; tsp_1; 5.
CC SMART; SM00303; GPS; 1.
CC SMART; SM00008; Hormr; 1.
CC SMART; SM00209; TSP1; 5.
CC PROSITE; PS0221; GPS; 1.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FALSE_NEG.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
CC PROSITE; PS02027; G_PROTEIN_RECEP_F2_3; 1.
CC PROSITE; PS02026; G_PROTEIN_RECEP_F2_4; 1.
CC PROSITE; PS00092; TSP1; 5.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC Repeat; Cell adhesion.
CC SIGNAL 1 30
FT CHAIN 31 1584
FT DOMAIN 31 948
FT TRANSMEM 949 969
FT DOMAIN 970 980
FT TRANSMEM 981 1001
FT DOMAIN 1002 1008
FT TRANSMEM 1009 1029
FT DOMAIN 1030 1052
FT TRANSMEM 1053 1073
FT DOMAIN 1074 1093
FT TRANSMEM 1094 1114
FT DOMAIN 1115 1136
FT TRANSMEM 1137 1157
FT DOMAIN 1158 1166
FT TRANSMEM 1167 1187
FT DOMAIN 1188 1584
FT DOMAIN 261 316
FT DOMAIN 354 408
FT DOMAIN 409 463
FT DOMAIN 467 521
FT DOMAIN 522 576
FT DOMAIN 581 938
FT DOMAIN 1411 1422
FT DOMAIN 1425 1430
FT SITE 231
FT DOMAIN 1365 1584
FT DOMAIN 1581 1584
FT CARBOHYD 64
FT CARBOHYD 401
FT CARBOHYD 607
FT CARBOHYD 692
POTENTIAL.
BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1.
EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
TSP TYPE-1 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 5.
GPS.
POLY-PRO.
POLY-PRO.
CELL ATTACHMENT SITE (POTENTIAL).
NECESSARY FOR INTERACTION WITH BAP1.
INDISPENSABLE FOR INTERACTION WITH BAP1.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).


```
QY 799 CWINNNAVFYTVVGVPCVIFLLNVSMFIVLVQLCRKIKKQKLGQAQRKTSIODLRSIAG 858
Db 293 DWHQAPVITVLAVN---LVFLSMMVLIITKLOSAENTAQQO---YRKAT-----KALLV 342
QY 859 LTFLLGTTWGFAPFAWGVNVNTEKMLF---AIFNTLQGGFFIFIFCYVAKENVK---908
Db 343 LFPLLGIT--YILMQGPMDCVAGHVFNAQALLSLQGGFTVALFYCFLENTEVONTLHRH 400
QY 909 -KQW-----RRYLCCGKRLAENSOWS-KTATNGLK 937
Db 401 MSRWRETRTVGGRRYTLTG-----HSKDWSPRSRSTESIR 435

RESULT 8
PACR_MOUSE STANDARD; PRT; 496 AA.
ID PACR_MOUSE
AC P70205;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide type I receptor
DE precursor (PACAP type I receptor) (PACAP-R-1).
GN ADCYAP1R1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=96255640; PubMed=8664310;
RA Hashimoto H., Yamamoto K., Hagiwara N., Ogawa N., Nishino A.,
RA Aino H., Nogi H., Imanishi K., Matsuda T., Baba A.;
RT "CDNA cloning of a mouse pituitary adenylate cyclase-activating
RT polypeptide receptor.";
RL Biochim. Biophys. Acta 1281:129-133(1996).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PACAP-27 AND PACAP-38. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE. MAY REGULATE THE RELEASE OF ADRENOCORTICOTROPIN,
CC LUTEINIZING HORMONE, GROWTH HORMONE, PROLACTIN, EPINEPHRINE, AND
CC CATECHOLAMINE. MAY PLAY A ROLE IN SPERMATOGENESIS AND SPERM
CC MOTILITY. CAUSES SMOOTH MUSCLE RELAXATION AND SECRETION IN THE
CC GASTROINTESTINAL TRACT.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; D82935; BAAL1639.1; -.
CC GCRDb; GCR_1152; -.
CC MGD; MGI:108449; Adcyap1r1.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G.PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G.PROTEIN_RECEP_F2_2; 1.
CC PROSITE; PS00651; G.PROTEIN_RECEP_F2_3; 1.
CC PROSITE; PS00652; G.PROTEIN_RECEP_F2_4; 1.
CC PROSITE; PS00653; G.PROTEIN_RECEP_F2_5; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC Spermatogenesis.
CC SIGNAL
CC CHAIN 1 20 POTENTIAL.
CC CHAIN 21 496 PITUITARY ADENYLATE CYCLASE ACTIVATING
CC DOMAIN 21 155 POLYPEPTIDE TYPE I RECEPTOR.
CC EXTRACELLULAR (POTENTIAL).
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FT TRANSMEM 156 178 1 (POTENTIAL).
FT DOMAIN 179 186 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 187 205 2 (POTENTIAL).
FT DOMAIN 206 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 228 253 3 (POTENTIAL).
FT DOMAIN 254 268 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 269 291 4 (POTENTIAL).
FT DOMAIN 292 309 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 310 332 5 (POTENTIAL).
FT DOMAIN 333 378 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 379 399 6 (POTENTIAL).
FT DOMAIN 400 413 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 414 433 7 (POTENTIAL).
FT DOMAIN 434 496 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 496 AA; 56639 MW; 47B5D51D4209060A CRC64;

Query Match 4.4%; Score 235; DB 1; Length 496;
Best Local Similarity 22.6%; Pred. No. 1.1e-05;
Matches 95; Conservative 75; Mismatches 145; Indels 106; Gaps 20;

QY 596 LQRNGRGWSD-----NGCSVKDRRLNETICTCSHLTSGVLLDLSRTSVLPQMMAL 649
Db 114 VGRNCTEDGSEFPFHYFDACGDDYE-----PESGDQDYIYLSV 153
QY 650 TPTITVIGCLSSIFSLVTLVYIAFEKIR--RDYPSKILIQCAALLILNLVFLDWSIA 707
Db 154 KALYTVGYSTSLVTLTAMVILCRFRKLHCTRNF---IHMNLFVSFMLRAISVFIKDWI- 209
QY 708 LYKMOGL-----CISVAVELHYFLVSTWMLGLEAFHMYLALVKVFTYRKYLK 758
Db 210 LYAEDSSHCFFVSTVECKAVMVFHYCVWSNYEFLTEGLYFLTLVETTFPE-RRFYW 268
QY 759 FCIVGKGVAVVVTI--ILTISPDNYCLGSGKPNCGSPDDFCWINNN--AVFYI---TV 811
Db 269 YTIIGWGTTCVTVWAVLRLYFDDAG-----CWMNDSTALWVVIKGPV 313
QY 812 VGYFCVIFLLNYSMTFVL-----VOLCRKIKKKQKLGQAQRKTSIOD 852
Db 314 VGSIMVNFVLFICILILVQKLOSPDMGNGESSIYFCVQKCYC--KQRAQQHCKMSE 371
QY 853 LRSI-----AGLIFLLGITWG--FAFFAWGVNVT--PMYLFAL-FNTLOGFEIFICYV- 902
Db 372 LSTITLRLARSTLLIPLFIHITVFAFSPENVSKRERLVFELGLGSGFGFVAVLYCFL 431
QY 903 ---AKENVKQWRRLCCGKRLAENSOWS---KTATNGLKKTQVNGVSSSSNSLOSS 955
Db 432 NGEVQAEIRKKRWSW---KVNRYFTWDFKRRHPSLASSGVNGGTQLSILSKSSQLRMS 487
QY 956 S 956
Db 488 S 488

RESULT 9
ID CRFL_SHEEP STANDARD; PRT; 415 AA.
AC O62772;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRFL)
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
GN CRHRL.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
```


G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 SIGNAL 1 ? POTENTIAL.
 CHAIN ? 413 CORTICOTROPIN RELEASING FACTOR RECEPTOR
 2.
 DOMAIN ? 120 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 121 141 1 (POTENTIAL).
 DOMAIN 142 150 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 151 170 2 (POTENTIAL).
 DOMAIN 171 187 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 188 211 3 (POTENTIAL).
 DOMAIN 212 225 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 226 247 4 (POTENTIAL).
 DOMAIN 248 266 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 267 289 5 (POTENTIAL).
 DOMAIN 290 312 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 313 332 6 (POTENTIAL).
 DOMAIN 333 347 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 348 367 7 (POTENTIAL).
 DOMAIN 368 413 CYTOPLASMIC (POTENTIAL).
 CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 413 AA; 48458 MW; DAD422F0A96C4626 CRC64;

Query Match 4.3%; Score 231.5; DB 1; Length 413;
 Best Local Similarity 23.3%; Pred. No. 1.4e-05;
 Matches 83; Conservative 63; Mismatches 127; Indels 83; Gaps 16;

QY 588 TVRCVFDLGRNGRGSGDNGSCVSKDRDLNETICPSHLTSFGLDLSRTSVLPQMM 647
 DB 78 .TTRNVYRCFENGWASW-----MNYSQCV-----PILDNKKYALHYKIA 118
 QY 648 ALTFITYGGLSIFLSVLTVYTAFAKIR--RDYPSKILIOALALLNLVFL-- 702
 DB 119 LI--INYLGHGISIALVIAFLFLCLRSICRLNT--IHNNLTITFLIRNMWFLQM 173
 QY 703 -----DSNIALYKMGGLGISVAVFLHYFLVFTWGLFAFMYLALVKVFN--YI 752
 DB 174 IDHNHESNEW-----CRCTITVYFVVTFFWFEVGCYLHTAIVTYSIDL 224
 QY 753 RYILKFCIVGVPV--VVTIITISPDNYGLSGYKPGPNPDDFCWNNNAVYIT 810
 DB 225 RKWV--FLFIGWCIPSPITVTAICKLFYEN-----EQCWIGKEPGYID 267
 QY 811 VV--GYFCVIFLLNMFVWLVLQCRKIKKOLGAQRKTSIOLRSIAG--LTFELGI 865
 DB 268 YIYOGRVILVLLN----FVFLNIVIRILMTKLRASTTETIQYRAKAVKATLVLLPLGI 323
 QY 866 TWGFAFFAWGPVNVV--FMYLFAIFNTLQGFIFIFYCVAKENV-----RKWRRY 914
 DB 324 TYMLFVNPGEDDVSOIVFIYFNSFLQSFQGFVSVFYCFNLNGEVSRAARKRWHRW 379

RESULT 11
 ID CRFL_RAT STANDARD; PRT: 415 AA.
 AC P35353;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRFL1)
 DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
 GN CRH1 OR CRHR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
 RX MEDLINE=94062694; PubMed=8243338;

Perrin M.H., Donaldson C.J., Chen R., Lewis K.A., Vale W.W.;
 "Cloning and functional expression of a rat brain corticotropin
 releasing factor (CRF) receptor.";
 Endocrinology 133:3058-3061(1993).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=SPRAGUE-DAWLEY;
 RX MEDLINE=9409969; PubMed=8274282;
 RA Chang C.P., Pearce R.V. II, O'Connell S., Rosenfeld M.G.;
 "Identification of a seven transmembrane helix receptor for
 corticotropin-releasing factor and sauvagine in mammalian brain.";
 Neuron 11:1187-1195(1993).
 [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Testis;
 RX MEDLINE=96278921; PubMed=8662941;
 RA Tsai-Morris C., Buczek E., Geng Y., Gamboa-Pinto A., Dufau M.L.;
 "The genomic structure of the rat corticotropin releasing factor
 receptor. A member of the class II G protein-coupled receptors.";
 J. Biol. Chem. 271:14519-14525(1996).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.
 CC SHOWS HIGH-AFFINITY CRF BINDING. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: ENTIRE NERVOUS SYSTEM.
 CC -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; L24096; ; NOT_ANNOTATED_CDS.
 DR EMBL; L25438; AAA16441.1; -.
 DR EMBL; U53498; AAC53519.1; -.
 DR EMBL; U53486; AAC53519.1; JOINED.
 DR EMBL; U53487; AAC53519.1; JOINED.
 DR EMBL; U53488; AAC53519.1; JOINED.
 DR EMBL; U53489; AAC53519.1; JOINED.
 DR EMBL; U53490; AAC53519.1; JOINED.
 DR EMBL; U53491; AAC53519.1; JOINED.
 DR EMBL; U53492; AAC53519.1; JOINED.
 DR EMBL; U53493; AAC53519.1; JOINED.
 DR EMBL; U53494; AAC53519.1; JOINED.
 DR EMBL; U53495; AAC53519.1; JOINED.
 DR EMBL; U53496; AAC53519.1; JOINED.
 DR EMBL; U53497; AAC53519.1; JOINED.
 DR GCRDB; GCR_0819; -.
 DR GCRDB; GCR_0947; -.
 DR GCRDB; GCR_1414; -.
 DR GCRDB; GCR_1415; -.
 DR GCRDB; GCR_1469; -.
 DR IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS02027; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS02061; G_PROTEIN_RECEP_F2_4; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Phosphorylation.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 415 CORTICOTROPIN RELEASING FACTOR RECEPTOR
 FT DOMAIN 25 121 1.
 FT TRANSMEM 122 142 1 (POTENTIAL).
 FT FT

FT DOMAIN 143 151 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 152 171 2 (POTENTIAL).
 FT DOMAIN 172 189 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 190 213 3 (POTENTIAL).
 FT DOMAIN 214 227 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 228 249 4 (POTENTIAL).
 FT DOMAIN 250 268 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 269 291 5 (POTENTIAL).
 FT DOMAIN 292 314 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 315 334 6 (POTENTIAL).
 FT DOMAIN 335 349 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 350 369 7 (POTENTIAL).
 FT DOMAIN 370 415 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 415 AA; 47842 MW; 48D6704B31D4C013 CRC64;

Query Match 4.3%; Score 230; DB 1; Length 415;
 Best Local Similarity 25.4%; Pred. No. 1.7e-05;
 Matches 103; Conservative 67; Mismatches 153; Indels 82; Gaps 22;

QY 543 QDPSLENLSIYVSSVANLTVRNLTNRVTTLKHNPSQDELTVR-C-----VFWD 595
 DB 26 QDQRCENLSL-----TSNVSLQC-NASVDLIGTCWPRSPA-QGLVVRPCPAFFYGVRYN 78
 QY 596 LGRNGGR-----GWSNDGCSVKDRLNCTICSHLTSGVLLDLSRTSVLPQMMALT 650
 DB 79 TTNGYRECLANGWA-----ARVNVSECO-----EILNEEKSKV---HYHVAV 120
 QY 651 FTIYIGCLSSIFLSTVLTVYIAFEKIR--RDYPSKILQICALLNLV-FLLDSWIA 707
 DB 121 YINVGHCIISVALLVAFLRLRSICRLNI---IHNWLSAFILRNATVFWVQLTVS 177
 QY 708 LYKMQ---GLCISVAVFLHYLLVSTWGLFAFMYLALVKVFNT-YIRKYLKFCIVG 763
 DB 178 PEVHQSNVACRLVTAAYVYHVTNFMFGEGCVLHTAIVLTSTDRLRKWM--FVCIG 235
 QY 764 WGV--PAVVVTIILTISPNDYGLSGYKFPNGSPDPCWINNNAVFYITVV--GYFCVIF 819
 DB 236 WGVFPPIIWAIGLHVDN-----EKWFGKRPVYTDYIYOGPMILVL 280
 QY 820 LNVSMFIVVLQCRKKKQKOLGAQRKTSIQDLRSIAG---LTFLLGITWGFAPFAWGP 876
 DB 281 LIN----FIFLNVIRIIMTKLRASSTTSETIQYRKAVKATLVLLPLGITYMLFFVNPGE 336
 QY 877 ---VNVTFMFLFAIFNTLOGFFIFIFVCV----AKENVKQWRY 914
 DB 337 DEYSRVVVFIFNSFLESFQGFVSVFYCLNSEVRSAIRKWRWR 381

RESULT 12
 ID PACR_BOVIN
 AC Q29627; STANDARD; PRT; 513 AA.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE pituitary adenylate cyclase activating polypeptide type I receptor
 DE precursor (PACAP type I receptor) (PACAP-R-1).
 DN ADCVAP1R.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 DX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;

RX MEDLINE-94325336; PubMed-8049255;
 RA Miyamoto Y., Habata Y., Ohtaki T., Masuda Y., Ogi K., Onda H.,
 RA Fujino M.;
 RT "Cloning and expression of a complementary DNA encoding the bovine
 RT receptor for pituitary adenylate cyclase-activating polypeptide
 RT (PACAP).";
 RL Biochim. Biophys. Acta 1218:297-307(1994).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR PACAP-27 AND PACAP-38. THE
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
 CC ADENYLATE CYCLASE. MAY REGULATE THE RELEASE OF ADRENOCORTICOTROPIN,
 CC LUTEINIZING HORMONE, GROWTH HORMONE, PROLACTIN, EPINEPHRINE, AND
 CC CATECHOLAMINE. MAY PLAY A ROLE IN SPERMATOGENESIS AND SPERM
 CC MOTILITY. CAUSES SMOOTH MUSCLE RELAXATION AND SECRETION IN THE
 CC GASTROINTESTINAL TRACT (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; A LONG FORM (SHOWN
 CC HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; D17290; BAA04122.1; -;
 CC EMBL; D17290; BAA04123.1; -;
 CC GCRDB; GCR_2658; -;
 CC GCRDB; GCR_2659; -;
 CC InterPro; IPR000832; GPCR_secretin.
 CC InterPro; IPR001879; hormn_receptor.
 CC Pfam; PF00002; 7tm_2; 1.
 CC Pfam; PF02793; HRM; 1.
 CC PRINTS; PR00249; GPCRSECRETIN.
 CC SMART; SM00008; HORMR; 1.
 CC PROSITE; PS00649; G-PROTEIN_RECP_F2_1; 1.
 CC PROSITE; PS00650; G-PROTEIN_RECP_F2_2; 1.
 CC PROSITE; PS02227; G-PROTEIN_RECP_F2_3; 1.
 CC PROSITE; PS02661; G-PROTEIN_RECP_F2_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Alternative splicing.
 FT SIGNAL 1 37
 FT CHAIN 38 513
 FT PITUITARY ADENYLATE CYCLASE ACTIVATING
 FT POLYPEPTIDE TYPE I RECEPTOR.
 FT EXTRACELLULAR (POTENTIAL).
 FT 1 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 2 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT 3 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 4 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT 5 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 6 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT 7 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 65 65
 FT CARBOHYD 77 77
 FT VARSPLIC 366 393 MISSING (IN SHORT ISOFORM).
 SQ SEQUENCE 513 AA; 58785 MW; 9A45753210CE9817 CRC64;

Query Match 4.3%; Score 228.5; DB 1; Length 513;
 Best Local Similarity 21.5%; Pred. No. 2.6e-05;
 Matches 107; Conservative 89; Mismatches 164; Indels 137; Gaps 25;

QY 521 PAH--DMELASRVQ--FNFFETPALFQDPSLENLSIYVSSVANLTVRNLTNRVTVL 577

Db	83	PAHVGEMVLVSCPELRIENPDQWE---TETIGFQFADSKSLDLMRVVSRNCT---	136
QY	578	KHNPISODELTVRCVFDLGRNGRGGWSO-----NGCSVKDRRLNETICTCSHLTSGF	631
Db	137	-----SETGDQDQYVLSVRLVGVYSTSLVTLTAMVILCRFRKLHCTRNF---IHMNL	209
QY	632	VLLDLRSVLPQAQMALFTVYIGCGLSIFLSTVLTYYIAFEKIR--RDYPSKILLIQL	689
Db	158	-----SETGDQDQYVLSVRLVGVYSTSLVTLTAMVILCRFRKLHCTRNF---IHMNL	209
QY	690	CAALLLNVLFLDLSIALYKMOGL-----CISVAVFLHYFLVSTFWMLGAEAFHM	740
Db	210	FVSMFLRAISVFTKDWI-LYAEQDSNHCFTSTVECKAVMFFHCVSVNYFWLFIEGLYL	268
QY	741	YLALVKVFNTYIRKYLKFCIVGNGVPAVVVTI--ILTISPDNYGLSGYKFPNGSPDDF	798
Db	269	FTLLVETFPPE-RRYFVWYIIIGWGTPTVCVSVWAMRLRYFDDTG-----	312
QY	799	CW--INNNAVFIY---TVVGYFCVIFLLNSMFIIVLVOLCR-----IKK	838
Db	313	CWDMNDNTALMWIKGVGVSIMVNFVLFIGI-IVILVQKLOSPDMGNGESSIYSCVOK	371
QY	839	---KKOLGAQRKTSIODLRST---AGLTFLGITWG--FAFFAWGPNVNT--FMYLFAL	887
Db	372	CYCKPQAOHQSCMSELSITLRLARSTLLIPLFEGHTYVFAFSPENSVKRERLVFEL	431
QY	888	-FNTLOGFFTFIYFCV-----AKENVKQWRRLYCCGKRLAENSWS-----KTA	938
Db	432	GLGSFGQFVAVLYCFLNGEYQAEIKRKRWSW---KVNRYFTMDFKHRHPSLASSGVNG	487
QY	939	QTVNQGVSSSSNSIOS 955	
Db	488	GTQLSILKSSSQIRMS 504	
RESULT 13			
PACR_HUMAN			
ID	PACR_HUMAN	STANDARD; PRT; 468 AA.	
AC	F41586;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Pituitary adenylate cyclase activating polypeptide type I receptor precursor (PACAP type I receptor) (PACAP-R-1).		
DE	ADCYAP1R.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Pituitary;		
RX	MEDLINE=94071918; PubMed=7902709;		
RA	Ogi K., Miyamoto Y., Masuda Y., Habata Y., Hosoya M., Ohtaki T.,		
RA	Masuo Y., Onda H., Fujino M.;		
RT	"Molecular cloning and functional expression of a cDNA encoding a		
RT	human pituitary adenylate cyclase activating polypeptide receptor.;"		
RL	Biochem. Biophys. Res. Commun. 196:1511-1521(1993).		
RN	[2]		
RP	SEQUENCE OF 418-468 FROM N.A.		
RC	TISSUE=Placenta;		
RX	MEDLINE=95154842; PubMed=7851900;		
RA	Stoffel M., Espinosa R., Trabb J.B., le Beau M.M., Bell G.I.;		
RT	"Human type I pituitary adenylate cyclase activating polypeptide		
RT	receptor (ADCYAP1R): localization to chromosome band 7p14 and		
RT	integration into the cytogenetic, physical and genetic map of		
RT	chromosome 7.;"		
RL	Genomics 23:697-699(1994).		
CC	-!- FUNCTION: THIS IS A RECEPTOR FOR PACAP-27 AND PACAP-38. THE		
CC	ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE		
CC	ADENYLATE CYCLASE. MAY REGULATE THE RELEASE OF ADRENOCORTICOTROPIN,		
CC	LUTEINIZING HORMONE, GROWTH HORMONE, PROLACTIN, EPINEPHRINE, AND		

C	C	CATECHOLAMINE. MAY PLAY A ROLE IN SPERMATOGENESIS AND SPERM	
C	C	MOTILITY. CAUSES SMOOTH MUSCLE RELAXATION AND SECRETION IN THE	
C	C	GASTROINTESTINAL TRACT.	
C	C	-!- SUBCELLULAR LOCATION: Integral membrane protein.	
C	C	-!- TISSUE SPECIFICITY: MOST ABUNDANT IN THE BRAIN, LOW EXPRESSION IN	
C	C	THE LUNG, LIVER, THYMUS, SPLEEN, PANCREAS AND PLACENTA.	
C	C	-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.	
C	C	-----	
C	C	This SWISS-PROT entry is copyright. It is produced through a collaboration	
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C	C	modified and this statement is not removed. Usage by and for commercial	
C	C	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
C	C	or send an email to license@isb-sib.ch).	
C	C	-----	
DR	EMBL; D17516; BAA04466.1; ALT_INIT.		
DR	EMBL; U09216; AAA19323.1; -.		
DR	GCRDB; GCR_0899; -.		
DR	MIM; 102981; -.		
DR	InterPro; IPR000832; GPCR_secretin.		
DR	InterPro; IPR001879; hormn_receptor.		
DR	Pfam; PF00002; 7tm_2; 1.		
DR	Pfam; PF02793; HRM; 1.		
DR	PRINTS; PR00249; GPCRSECRETIN.		
DR	SMART; SM00008; HORMR; 1.		
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.		
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.		
DR	PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.		
DR	PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;		
KW	Spermatogenesis.		
FT	SIGNAL	1 20	POTENTIAL.
FT	CHAIN	21 468	PITUITARY ADENYLATE CYCLASE ACTIVATING
FT			POLYPEPTIDE TYPE I RECEPTOR.
FT			EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	21 155	1 (POTENTIAL).
FT	TRANSMEM	156 178	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	179 186	2 (POTENTIAL).
FT	TRANSMEM	187 205	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	206 227	3 (POTENTIAL).
FT	TRANSMEM	228 253	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	254 268	4 (POTENTIAL).
FT	TRANSMEM	269 291	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	292 309	5 (POTENTIAL).
FT	TRANSMEM	310 332	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	333 350	6 (POTENTIAL).
FT	TRANSMEM	351 371	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	372 385	7 (POTENTIAL).
FT	TRANSMEM	386 405	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	406 468	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	48 48	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	60 60	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	117 117	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	300 300	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	375 375	N-LINKED (GLCNAC. .) (POTENTIAL).
QY	SEQUENCE	468 AA; 53313 MW; BB515B84E9F28977 CRC64;	
QY	595	DLG---RNGRGWSD-----NGCSVKDRRLNETICTCSHLTSGVLLDLSTSVLPAQ	645
Db	110	DMGVSVNRCTEDGWSEPFPHFYDACGDEVE-----SETGDQDY 149	
QY	646	MMALFTFTYIGCGLSIFLSTVLTYYIAFEKIR--RDYPSKILLIQLCALLLNLVFLLD	703
Db	150	YLSVKALYTVGYSTSLVTLTAMVILCRFRKLHCTRNF---IHMNLFSFMLRAISVFIK	206
QY	704	SWIALYKMOGL-----CISVAVFLHYFLVSTFWMLGAEAFHMYLALVKVFNTYIRK	754
Db	207	DWI-LYAEQDSNHCFTSTVECKAVMFFHCVSVNYFWLFIEGLYFLVLTVEFPE-RR	264

Query Match 4.3%; Score 227.5; DB 1; Length 468;
Best Local Similarity 23.0%; Pred. No. 2.6e-05;
Matches 91; Conservative 74; Mismatches 151; Indels 79; Gaps 18;

```

RESULT 15
VIPR_RAT
VIPR_RAT
ID VIPR_RAT STANDARD; PRT; 459 AA.
AC P30083:
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE vasoactive intestinal polypeptide receptor 1 precursor (VIP-R-1)
DE (Pituitary adenylate cyclase activating polypeptide type II receptor)
DE (PACAP type II receptor) (PACAP-R-2).
DE VIPR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=923232309; PubMed=1314625;
RA Ishihara T., Shigemoto R., Mori K., Takahashi K., Nagata S.;
RT "Functional expression and tissue distribution of a novel receptor
for vasopressin in the rat brain."
RL Neuron 8:811-819(1992).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: IN LIVER, LUNG, INTESTINES, THYMUS AND BRAIN
CC (MOSTLY IN THE CEREBRAL CORTEX AND HIPPOCAMPUS).
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M86835; AAA42331.1; -;
CC PIR: JH0594; JH0594.
CC GCRD: GCR_0369; -;
CC InterPro: IPR000832; GPCR_secretin.
CC InterPro: IPR001879; hormn_receptor.
CC Pfam: PF00002; 7tm.2; 1.
CC Pfam: PF02793; HRM; 1.
CC PRINTS: PR00249; GPCRSECRETIN.
CC SMART: SM00008; Hormr; 1.
CC PROSITE: PS00649; G-PROTEIN_RECEP_F2.1; 1.
CC PROSITE: PS00650; G-PROTEIN_RECEP_F2.2; 1.
CC PROSITE: PS00227; G-PROTEIN_RECEP_F2.3; 1.
CC PROSITE: PS00261; G-PROTEIN_RECEP_F2.4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
KW SIGNAL
FT CHAIN 1 30
FT VASOACTIVE INTESTINAL POLYPEPTIDE
FT RECEPTOR 1.
FT 1 143
FT DOMAIN 31 143
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 168
FT TRANSMEM 169 175
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 176 195
FT 2 (POTENTIAL).
FT TRANSMEM 196 217
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 218 241
FT 3 (POTENTIAL).
FT TRANSMEM 242 255
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 256 277
FT 4 (POTENTIAL).
FT TRANSMEM 278 294
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 318
FT 5 (POTENTIAL).
FT TRANSMEM 319 343
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 344 363
FT 6 (POTENTIAL).
FT TRANSMEM 364 375
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 376 395
FT 7 (POTENTIAL).
FT TRANSMEM 396 459
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 459 488
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 58 58
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 69 69
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 459 AA; 52057 MW; 99E8957DA86698D2 CRC64;
Query Match 4.2%; Score 223.5; DB 1; Length 459;
Best Local Similarity 23.0%; Pred. No. 4.2e-05;
Matches 94; Conservative 68; Mismatches 163; Indels 83; Gaps 16;
QY 594 WDLGRNGRGGRGSD-----NCGSKVDRRLNETICTCSHLTSFGVLIDLSRTSVLPQAM 646
DB 99 YNISRCTEGSQLEPGPHIACGLND-----RASSLDEQ 135

QY 647 MALTFITY-----IGCGLSSIFSLVTLVYIAFEKIR--RDYPSKILIQCAALLNLV 699
DB 136 QTFEYNTVKYGTTCYSLSLASLLVAMAILSLFRHLCTRTNVIHMLFW--SFILRATA 193
QY 700 FLDSWIALYKMOGL-----CISVAVFLHYFLYSFTWMGLEAFHMYLALVKVENT 750
DB 194 FKID--MALFNSGEIDHCSEASVGCCKAAVFFQYCVMANFFWLLVEGLYLYTLVASFFS 251
QY 751 YIRKYLKFCIVGKGVPAVVVTI--ILRISPDNYGLGSKYCKFPNGSPDDFCW--INNAN 806
DB 252 E-RKFFWGYILLIGMGVPSVFTITWTIVRIYFDFG-----CWDTIINSSL 295
QY 807 FYITVVGVCVIFLLNVSMFIVLVOLCRKKKOLGAORQTSIQDLRSIAGTLFLLGIT 866
DB 296 WWI--IKAPILLSILNVFLFCIRILVQLRPDIDG---KNDSSPSYSLAKSTLLLIPL 351
QY 867 WG--FAFAWGPVNV---TFMYLFAIFNTLQGFIFEFYCV-----AKENVKRWKRRWLQ 411
DB 352 FGIHYVMAFFPDNFKAQVKVFFELVVGSGFQGVVAILCYFLNGEVAQLRRKRRHQL 965
QY 918 GKRLAENSWSKATNGLLKQTVNQGVSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 917
DB 412 GVLGSSSKSQHPGWSNGATCTQVSMLTRVSPSARRSSSFQAEVSLV 459

RESULT 16
MTHL DROME STANDARD; PRT; 676 AA.
AC Q9VXD9;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Probable G-protein-coupled receptor Mth-like 1 precursor (Methuselah-
DE like 1 protein).
GN MTHL1 OR CG4521.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Basley E.M.,
RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hartis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RESULT 18
 DTHR_MANSE
 AC P35464; STANDARD; PRT; 395 AA.
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Diuretic hormone receptor (DH-R).
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94103310; PubMed=8276884;
 RA Reagan J.D.;
 RT "Expression cloning of an insect diuretic hormone receptor. A member
 of the calcitonin/secretin receptor family.";
 RL J. Biol. Chem. 269:9-12(1994).
 CC -!- FUNCTION: RECEPTOR FOR THE INSECT DIURECTIC HORMONE. THE ACTIVITY
 OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE
 CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN MALPIGHIAN TUBULES.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL; U03489; AAC46469.1; -;
 CC GCRDB; GCR 0644; -;
 CC InterPro; IPR000832; GPCR_secretin.
 CC InterPro; IPR001879; hormn_receptor.
 CC Pfam; PF00002; 7tm_2; 1.
 CC Pfam; PF02793; HRM; 1.
 CC PRINTS; PR00249; GPCRSECRETIN.
 CC SMART; SM00008; Hormr; 1.
 CC PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 CC PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 CC PROSITE; PS00651; G_PROTEIN_RECP_F2_3; 1.
 CC PROSITE; PS00652; G_PROTEIN_RECP_F2_4; 1.
 CC PROSITE; PS00653; G_PROTEIN_RECP_F2_5; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 CC DOMAIN 1 87 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 88 111 1 (POTENTIAL).
 CC DOMAIN 112 119 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 120 140 2 (POTENTIAL).
 CC DOMAIN 141 155 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 156 176 3 (POTENTIAL).
 CC DOMAIN 177 195 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 196 217 4 (POTENTIAL).
 CC DOMAIN 218 248 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 249 272 5 (POTENTIAL).
 CC DOMAIN 273 295 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 296 314 6 (POTENTIAL).
 CC DOMAIN 315 329 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 330 349 7 (POTENTIAL).
 CC DOMAIN 350 395 CYTOPLASMIC (POTENTIAL).
 CC CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 395 AA; 45420 MW; 3F8C1A3EFA01B2D CRC64;

Query Match 4.1%; Score 219; DB 1; Length 395;
 Best Local Similarity 25.6%; Pred. No. 6e-05;
 Matches 87; Conservative 62; Mismatches 117; Indels 74; Gaps 21;
 QY 643 PAOMMALTEITYICGSLSSIFSLVTLVYIAFEKTR-----RDYPSKILILQALALL 695
 Db 82 PTDVASLIYLA--GYSLSLAVLSLAVFVFLYFKDLRCLRNTHTNLMSTYLSACS--WI 137
 QY 696 LNLVFLDLSWI-ALYKMOGLCTISVAVFLVLLVFTWMLGLFAFHMALVLYKVF--NTY 751
 Db 138 LNLV--LQNSDESQODTSCMILVICNNYFVLTNFFMVLVEGLIYLMVVEFTAEINIK 195
 QY 752 IRKYLKFCIVGCVPAVVVVI-----ILTISPONYGLSGYKPPNGSPDDFC--WINNN 804
 Db 196 LKVI-----TTTGWGAPAVFITWISRCFVNVLPST-GPDGLAMFPEAK---MCIWMHEH 247
 QY 805 AVEFYI-----TWVGYFCVIFLLNVSFIVLVOLCRKKKKKOLGAORKTSTQDLRSAGLT 860
 Db 248 QVDWIHKAPALVGLALNLFLLIRIMW--VLTKLRASANTLETEQYRKAT----KALLVLI 301
 QY 861 FILGIT-----WGFAFWGPNVNTFMYLFAIFNTLQGGFFIFIFCYCAKENVR 908
 Db 302 PLLGITNLLVLCGSPDDSW-FAY-----AFDYTRALMLSTQGTVALFYCFMTEVR 352
 QY 909 -----KOWR--RYLCCGKLRLAENS-DWS-KTATNGLK 937
 Db 353 HAIRYHVERWKTGTIGGRRRGASYSKDWSPRSKTESIR 392
 RESULT 19
 CRF1_HUMAN
 ID CRF1_HUMAN STANDARD; PRT; 444 AA.
 AC P34598; Q13008; Q9UK64;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
 DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=pituitary;
 RX MEDLINE=94022296; PubMed=7692441;
 RA Chen R., Lewis K.A., Perrin M.H., Vale W.W.;
 RT "Expression cloning of a human corticotropin-releasing-factor
 receptor.";
 RT Proc. Natl. Acad. Sci. U.S.A. 90:8967-8971(1993).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94063063; PubMed=8243652;
 RA Vita N., Laurent P., Lefort S., Chalon P., Lelias J.-M., Kaghad M.,
 le Fur G., Caput D., Ferrara P.;
 RT "Primary structure and functional expression of mouse pituitary and
 human brain corticotropin releasing factor receptors.";
 RL FEBS Lett. 335:1-5(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Sakai K., Yamada M., Horiba N., Wakui M., Demura H., Suda T.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM CRF-R3).
 RC TISSUE=Hippocampus;
 RX MEDLINE=95110332; PubMed=7811272;
 RA Ross P.C., Kostas C.M., Ramabhadran T.V.;
 RT "A variant of the human corticotropin-releasing factor (CRF)
 receptor: cloning, expression and pharmacology.";
 RL Biochem. Biophys. Res. Commun. 205:1836-1842(1994).

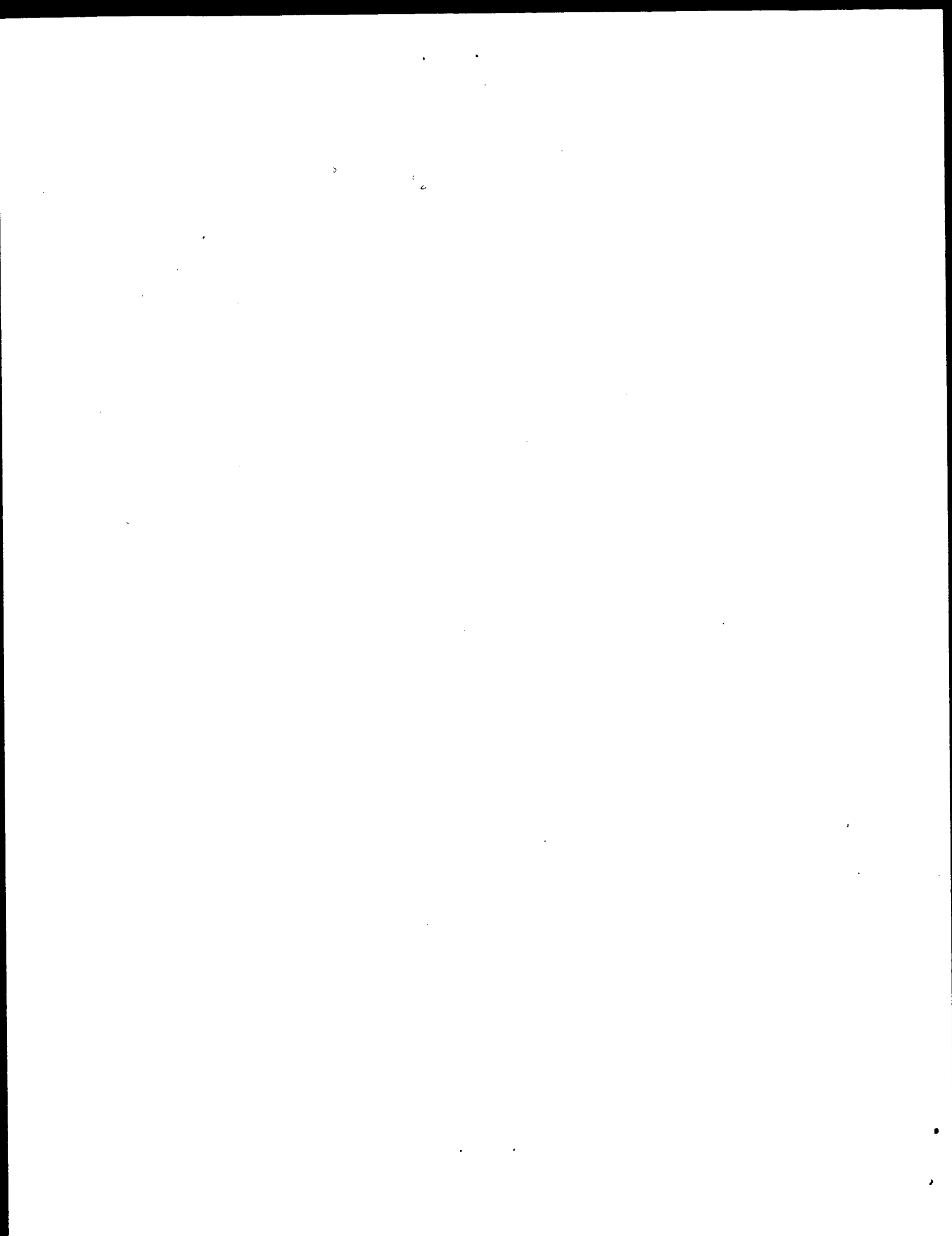
TRANSMEM	175	194	2 (POTENTIAL).
DOMAIN	195	216	EXTRACELLULAR (POTENTIAL).
TRANSMEM	217	240	3 (POTENTIAL).
DOMAIN	241	254	CYTOPLASMIC (POTENTIAL).
TRANSMEM	255	276	4 (POTENTIAL).
DOMAIN	277	292	EXTRACELLULAR (POTENTIAL).
TRANSMEM	293	316	5 (POTENTIAL).
DOMAIN	317	341	CYTOPLASMIC (POTENTIAL).
TRANSMEM	342	361	6 (POTENTIAL).
DOMAIN	362	373	EXTRACELLULAR (POTENTIAL).
TRANSMEM	374	393	7 (POTENTIAL).
DOMAIN	394	457	CYTOPLASMIC (POTENTIAL).
CARBOHYD	58	58	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	69	69	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	100	100	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
VARSPLIC	1	32	MRPSPPLPAPMCVCLAGLAWALGAGQAAR -> MPFPF
			LLRSVRLRGGMVSAVRLVVAAGASRGSGRGSGAGGGGR
			GGVARRRLRLAARSLGLGS (IN LONG ISOFORM).
SEQUENCE	457 AA:	51547 MW:	DAA40CF5BEC47D7D CRC64:
ISO			

Query Match	3.9%	Score 208;	DB 1;	Length 457;
Best Local Similarity	24.1%	Pred. No. 0.00028;		
Matched	94.	Mismatched	167;	Indels 74;
Conservative				Gaps 15;

QY	646	MMALTFITYICGGLSSIFLSVTLVTYIAFEKTR--RDYPSK---ILIQCAALLLNLFV	700
Db	143	KTGYT----IGYGLSLATLLVATALLSFRKHUCTRNYTHMLHFISETLRAAAVFKDLA	198
QY	701	LLDSWIALYKMOGL--CISVAFELHYFLVLSVTWGLEAFHMYLALVKVFNTRYIRYLK	758
Db	199	LPSGESDQSEGSVGCKAAMVFOQYCVMANFEWLLVEGLYLTLLAVSFSE-RKYFWG	257
QY	759	FCIVGWGVA--VVVTIILTSPDNWGLSGYKGFNGSPDDPCWNNNAVFTYTVGYFC	816
Db	258	YILIGWGPSTFMVWTIARHFEDYG-----CWDITNSLWIIKGPIL	302
QY	817	VIFLLNYSMFIVLVOLCRIKKKOLGAORKTSIQDLRSIAGITELLGITWG--FAFEAW	874
Db	303	TSILNVNFIETCIIRILLQKLRPPDI---RKSDSPYSRLARSTLLIPLUGVHYINFAF	359
QY	875	GPVNV--TEMYLFAIENTLOGEFTIFYCYV---AKENVRKORWRYLCCGKRLAENS	927
Db	360	FPDNFKPEVKMVFELVVGSGFVAILCYFLNGEYQAEELRRKWRWHLOQVLGWNPKYR	419
QY	928	WSKTATNGLKKQT-----VNQGVSSSN	950
Db	420	HPSGSGNCACTCSTOVSMLTRYSPGARRSS	449

81:

RESULT	24
SCRC_RABBIT	
ID	SCRC.RABBIT
AC	O46502;
DT	15-JUL-1999 (Rel. 38, Created)
DT	15-JUL-1999 (Rel. 38, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Secretin receptor precursor (SCT-R).
GN	SCTR;
OS	Oryctolagus cuniculus (Rabbit).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX	NCBI_TaxID=9986;
RN	[1]
RX	SEQUENCE FROM N.A.
RA	MEDLINE=98366112; PubMed=9700755;
RA	Vsoboda M., Tastyenoy M., de Neef P., Delporte C., Waelbroeck M.,
RA	Robberecht P.;



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2002, 07:35:41 ; Search time 40.63 seconds
(without alignments)
4419.610 Million cell updates/sec

Title: US-09-731-657-2

Perfect score: 5352

Sequence: 1 SQPEDASGRCAQRFSTLFE.....GRMALRRTSKRSLHFTQEQM 1038

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

- 1: SP TREMBL_19.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5232	97.8	1014	4	O00406
2	1372.5	25.6	512	4	Q96JW0
3	1368.5	25.6	541	4	Q9Y3K0
4	651.5	12.2	687	11	Q902H2
5	629	11.8	687	4	Q95966
6	618	11.5	693	4	Q96HB4
7	617.5	11.5	693	4	Q91653
8	589	11.0	823	4	Q90HX3
9	539	10.1	1403	4	Q95490
10	536.5	10.0	1283	6	Q97823
11	536.5	10.0	1351	6	Q97829
12	536.5	10.0	1512	6	Q97821
13	536.5	10.0	1580	6	Q97827
14	536	10.0	1527	11	O88927
15	534	10.0	1274	6	Q97820
16	534	10.0	1342	6	Q97826

17	534	10.0	1450	6	O97811	O97811 bos taurus
18	534	10.0	1503	6	O97818	O97818 bos taurus
19	534	10.0	1571	6	O97824	O97824 bos taurus
20	533.5	10.0	1240	6	O97822	O97822 bos taurus
21	533.5	10.0	1308	6	O97828	O97828 bos taurus
22	533	10.0	872	4	O94867	O94867 homo sapien
23	531.5	9.9	1407	6	O97810	O97810 bos taurus
24	531.5	9.9	1550	11	O92173	O92173 rattus norv
25	531	9.9	1231	6	O97819	O97819 bos taurus
26	531	9.9	1299	6	O97825	O97825 bos taurus
27	530.5	9.9	1177	4	O9UKY6	O9UKY6 homo sapien
28	530	9.9	1021	4	O94882	O94882 homo sapien
29	528.5	9.9	1465	6	O97813	O97813 bos taurus
30	527.5	9.9	1463	6	O97815	O97815 bos taurus
31	526	9.8	1240	4	O9HAR2	O9HAR2 homo sapien
32	526	9.8	1422	6	O97812	O97812 bos taurus
33	525	9.8	1420	6	O97814	O97814 bos taurus
34	522	9.8	1123	4	O9UKY5	O9UKY5 homo sapien
35	522	9.8	1478	6	O97817	O97817 bos taurus
36	520.5	9.7	1384	6	O97803	O97803 bos taurus
37	519.5	9.7	1435	6	O97816	O97816 bos taurus
38	518	9.7	1341	6	O97802	O97802 bos taurus
39	517	9.7	1449	5	Q10922	Q10922 caenorhabdi
40	515	9.6	1399	6	O97805	O97805 bos taurus
41	514	9.6	1397	6	O97807	O97807 bos taurus
42	512.5	9.6	1356	6	O97804	O97804 bos taurus
43	511.5	9.6	1354	6	O97806	O97806 bos taurus
44	508.5	9.5	1412	6	O97809	O97809 bos taurus
45	507.5	9.5	986	5	Q9N9W3	Q9N9W3 haemochus
46	506.5	9.5	2144	11	Q9QYP2	Q9QYP2 rattus norv
47	506	9.5	1369	6	O97808	O97808 bos taurus
48	505	9.4	1467	6	O97830	O97830 bos taurus
49	505	9.4	1472	6	O97831	O97831 bos taurus
50	503.5	9.4	1469	4	O9HAR3	O9HAR3 homo sapien
51	503.5	9.4	1474	4	O94910	O94910 homo sapien
52	501.5	9.4	652	4	O9BY15	O9BY15 homo sapien
53	500.5	9.4	1478	11	O88923	O88923 rattus norv
54	498	9.3	1487	11	Q92174	Q92174 rattus norv
55	495.5	9.3	2920	11	Q9F0M0	Q9F0M0 mus musculu
56	494	9.2	1515	11	O88917	O88917 rattus norv
57	494	9.2	2408	4	Q92566	Q92566 homo sapien
58	494	9.2	2923	4	Q9HCU4	Q9HCU4 homo sapien
59	493.5	9.2	732	6	Q95162	Q95162 sus scrofa
60	491.5	9.2	835	4	O00718	O00718 homo sapien
61	489	9.1	899	11	Q99K26	Q99K26 mus musculu
62	476.5	8.9	738	11	Q91W44	Q91W44 mus musculu
63	472	8.8	722	11	Q9DC42	Q9DC42 mus musculu
64	472	8.8	724	11	Q923A1	Q923A1 mus musculu
65	471.5	8.8	986	4	O94858	O94858 homo sapien
66	471	8.8	884	11	Q922R4	Q922R4 mus musculu
67	470.5	8.8	1346	4	Q9U1Z3	Q9U1Z3 homo sapien
68	468	8.7	1318	4	Q9H1S2	Q9H1S2 homo sapien
69	467	8.7	724	11	Q9JLQ8	Q9JLQ8 mus musculu
70	467	8.7	739	11	Q923X1	Q923X1 mus musculu
71	463.5	8.7	999	4	Q9H1S1	Q9H1S1 homo sapien
72	463	8.7	344	4	Q9Y4B1	Q9Y4B1 homo sapien
73	463	8.7	738	11	Q9ESC1	Q9ESC1 rattus norv
74	462.5	8.6	797	4	Q96K78	Q96K78 homo sapien
75	462	8.6	818	11	Q9Z0M6	Q9Z0M6 mus musculu
76	459.5	8.6	1092	4	Q9H1S4	Q9H1S4 homo sapien
77	458	8.6	606	4	Q9HBW9	Q9HBW9 homo sapien
78	457.5	8.5	839	4	Q96IE7	Q96IE7 homo sapien
79	457	8.5	689	11	Q91ZE5	Q91ZE5 mus musculu
80	457	8.5	3034	11	Q35161	Q35161 mus musculu
81	452	8.4	1014	5	O17505	O17505 caenorhabdi
82	451	8.4	1038	4	Q9H1S3	Q9H1S3 homo sapien
83	447	8.4	1477	4	O95722	O95722 homo sapien
84	447	8.4	3014	4	O9NYQ6	O9NYQ6 homo sapien
85	420.5	7.9	3301	11	O91Z10	O91Z10 mus musculu
86	410	7.7	1349	11	O9WVW0	O9WVW0 rattus norv
87	406	7.6	774	5	Q9VA13	Q9VA13 drosophila
88	405.5	7.6	3313	11	O88278	O88278 rattus norv
89	397	7.4	1364	4	O75092	O75092 homo sapien


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Db 541 TVNLNRNVTTLKHNPSODELVRCVFDLGRNGRGWSDNGCSVKDRRLNETICTC 600
QY 625 SHLTSGVLLDLRSRTSVLPQAMMALTFITYIGCGLSIFLSVTLTYIAFEKIRRDYPSK 684
Db 601 SHLTSGVLLDLRSRTSVLPQAMMALTFITYIGCGLSIFLSVTLTYIAFEKIRRDYPSK 660
QY 685 ILIQCAALLLNLFVLLDSWIALYKMGGLCSISAVFLHYFLVFTWMLGFAFMYLAL 744
Db 661 ILIQCAALLLNLFVLLDSWIALYKMGGLCSISAVFLHYFLVFTWMLGFAFMYLAL 720
QY 745 KVVFNTYIRKYILKFCIVGVPVAVVTIILTISPDNYGLSGYKFPNGSPDDFCWNN 804
Db 721 KVVFNTYIRKYILKFCIVGVPVAVVTIILTISPDNYGLSGYKFPNGSPDDFCWNN 780
QY 805 AVFYITVVGFCYFIFLLNVSMFIVVLVOLCRKKKQKQAGKRTSIQDLRSIAGLTFLLG 864
Db 781 AVFYITVVGFCYFIFLLNVSMFIVVLVOLCRKKKQKQAGKRTSIQDLRSIAGLTFLLG 840
QY 865 ITWGAFFAFWANGPVNVTMYLFAIPNTLOGFFIFICYVAKENVRKOWRRLCCGKLRLAE 924
Db 841 ITWGAFFAFWANGPVNVTMYLFAIPNTLOGFFIFICYVAKENVRKOWRRLCCGKLRLAE 900
QY 925 NSDWSKTATNGLKQKQVNOGVSSSSNSLQSSNSTTLLVNDSCVHASNGNASTER 984
Db 901 NSDWSKTATNGLKQKQVNOGVSSSSNSLQSSNSTTLLVNDSCVHASNGNASTER 960
QY 985 NGVSFVQNGDVCLHDFGTGKHMFENEKSCNGKRMALRRTSKRGLHFIFQOM 1038
Db 961 NGVSFVQNGDVCLHDFGTGKHMFENEKSCNGKRMALRRTSKRGLHFIFQOM 1014

RESULT 2
Q96JW0 PRELIMINARY; PRT; 512 AA.
ID Q96JW0 AC
AC Q96JW0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FLJ14937 FIS, CLONE PLACE1010231, WEAKLY SIMILAR TO CELL
DE SURFACE GLYCOPROTEIN EMRI PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,
RA Wagaatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Takiguchi S.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Nanomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027843; BAB55406.1; -.
SQ SEQUENCE 512 AA; 57870 MW; BB4EC50BF3FCDDBE CRC64;

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Query Match 25.6%; Score 1372.5; DB 4; Length 512;
 Best Local Similarity 52.6%; Pred. No. 2.4e-88;
 Matches 266; Conservative 89; Mismatches 124; Indels 27; Gaps 11;

```

QY 507 IGTITLPSLLMNNLPAHDMELASRVQNFETPALFDPSLENLSLYVTSSSVANLTV 566
Db 11 LASVILPNLLENLSPEDSVLVRRAGFTFENKLTGLQDVGPQRKTLVSYVMACSGNITI 70
QY 567 RNLTRNVTTLKHNPSODELVRCVFDLGRNGRGWSDNGC-SYKDRRLNETICTCS 625
Db 71 QNLKDPVOIKIKHTTQEVHHP1-CAFWDLNKNKSGFWNTSGCAVHRSDASSETVCLCN 129

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QY 626 HLTSFGVLLDLRSRT-SVLPAQ-MMALTFITYIGCGLSIFLSVTLTYIAFEKIRRDYPS 683
Db 130 HTHFGVLLDPLRSASQDARNTKVLTFISYIGCGISAIFSAATLLTYVAFEKLRDRDPS 189
QY 684 KILIQCAALLLNLFVLLDSWIALYKMGGLCSISAVFLHYFLVFTWMLGFAFMYLAL 743
Db 190 KILMNLSTALLFNLLFLDGLWITSFNVNGLGCIACVAVLLHFFELLATFTWMLGFAFMYIA 249
QY 744 LVKVFNTYIRKYILKFCIVGVPVAVVTIILTISPDN--YGLSGYKFPNGSPDDFCWI 801
Db 250 LVKVFNTYIRRYILKFCIIIGMGLPALVSVVLASNNNEVYKESYK---EKGDFFCWI 306
QY 802 NNAVEYITVVGFCYFIFLLNVSMFIVVLVOLCRKKKQKQAGKRTSIQDLRSIAGLTF 861
Db 307 QDPVIFYVTCAGYGVNFFLNAMFIVVVOICGNGRGRSRTLREEVLRNLSVSLTF 366
QY 862 LGITWGAFFAFWANGPVNVTMYLFAIPNTLOGFFIFICYVAKENVRKOWRRLCCGKLRL 921
Db 367 LLGMTWGAFFAFWANGPLNIPMYLFSIFNSLQGLFIFIEHCAMKENVKQWRRLCCGRPR 426
QY 922 LAENSWSKTATNGLKQKQVNOGVSSSSNSLQSS-----NSTSTLLVNDSCVHAS 975
Db 427 LADNSWSKTATNIIKKSDNLKSLSSSGNSTYLTSSKSSSTTYFKRN-----S 480
QY 976 GNGNASTERNVGSFVQNGDV--CLH 999
Db 481 HTDNVSYEH--SFN-KSGSLRQCFH 502

RESULT 3
Q9Y3K0 PRELIMINARY; PRT; 541 AA.
ID Q9Y3K0 AC
AC Q9Y3K0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DJ287G14.2 (PUTATIVE NOVEL SEVEN TRANSMEMBRANE DOMAIN PROTEIN)
DE (FRAGMENT).
GN DJ287G14.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mashreghi-Mohammadi M.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL033377; CAB42901.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR000203; PKD_cys-rich.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF01825; GPS; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00303; GPS; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
KW Transmembrane.
FT NON_TER 1
SQ SEQUENCE 541 AA; 61048 MW; 0672C54BEEC7E91D CRC64;

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Query Match 25.6%; Score 1368.5; DB 4; Length 541;
 Best Local Similarity 52.2%; Pred. No. 4.8e-88;
 Matches 261; Conservative 92; Mismatches 126; Indels 21; Gaps 8;

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QY 507 IGTITLPSLLMNNLPAHDMELASRVQNFETPALFDPSLENLSLYVTSSSVANLTV 566
Db 11 LASVILPNLLENLSPEDSVLVRRAGFTFENKLTGLQDVGPQRKTLVSYVMACSGNITI 70
QY 567 RNLTRNVTTLKHNPSODELVRCVFDLGRNGRGWSDNGC-SYKDRRLNETICTCS 625
Db 71 QNLKDPVOIKIKHTTQEVHHP1-CAFWDLNKNKSGFWNTSGCAVHRSDASSETVCLCN 129
QY 626 HLTSFGVLLDLRSRT-SVLPAQ-MMALTFITYIGCGLSIFLSVTLTYIAFEKIRRDYPS 683

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Db 130 HETFGVMDLPRSAQOLDARNTKVLTFISYIGCGISAIFAATLTLTVAPEKLRDIPS 189
QY 684 KILIOCAALLLNFLDLSWIALYKMGICISAVFVFLHYFLVLSFTWMGLEAFHMYLA 743
Db 190 KILMNSTALLFLNLLDGGWITSFNVGDLGCIADVALLHFFELLATFTWMGLEAHMYTA 249
QY 744 LKVFNTYIRKYILKFCIVGCVGPAVVVITILTSPDN--YGLSGYKFPNGSPDDFCWI 801
Db 250 LKVFNTYIRKYILKFCIVGCVGPAVVVITILTSPDN--YGLSGYKFPNGSPDDFCWI 306
QY 802 NNNAVFIYVGVFCVFLNLSMFIVVLVOLCRKKKOLGAORKTSTODLRSIAGLTF 861
Db 307 QDPVIEFVTCAGVGVNMFELNIAFIVVMVGICGRNGRKNRTLREELVRLNRSVSLTF 366
QY 862 LLGITGFAFFAGPVNVTMYLFAINTLOGFFIFICYVAKENVRKOWRYLCGKLR 921
Db 367 LLGWTGFAFFAGPLNIPENYLFISNLOGLFIIFHCAMKENVQKWRQHLCGRFR 426
QY 922 LAENSDWKTATNGLKKQTVNOGVSSSSNSLOSS-----NSTNSTLLVNDSCVHAS 975
Db 427 LADNSDWSKTATNIKKSSDNLGKSSSGNSTYLTSSKSSSTTYEKKR-----S 480
QY 976 GNGNASTERNGVSPFVQNGD 995
Db 481 HTDSASMDKSLSLAHADGD 500

RESULT 4
Q0Q2T2 PRELIMINARY; PRT; 687 AA.
AC Q0Q2T2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SERPENTINE RECEPTOR.
GN GPR56 OR Cyt28.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=LIVER;
RA Phillips R.L., Ernst R.E., Dosil M., Wesley C.K., Moore K.A.,
RA Kingsley P.D., Sykes S., Pallas J., Lemischka I.R.;
RT "Identification of novel hematopoietic stem cell regulatory genes.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF166382; AAF00617.1; -.
DR MGD; MGI:1340051; Gpr56.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF01825; GPS; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00303; GPS; 1.
DR PROSITE; PS00455; AMP_BINDING; UNKNOWN_1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 687 AA; 77271 MW; B5315D70AF443809 CRC64;

Query Match 12.2%; Score 651.5; DB 11; Length 687;
Best Local Similarity 28.2%; Pred. No. 1.8e-37;
Matches 174; Conservative 118; Mismatches 258; Indels 67; Gaps 16;

QY 342 QSETISSPMPOTHVSGTPPVKASRSPVSPAPANTVTSAPPVQDVTIVTSSISDLENQ 401
Db 127 QSLKQAGPLIATSVSSQWIPQNTSLP-----GAPSFIFSHNAPHKVSHNASVDMCDLKE 182
QY 402 VLQMEKALSLGSLPLENLAGEMTNQVSRLLHSPDML-APLAQRLLKVVDIGLQNFNT 460

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Db 183 -----LQQLSRYLQHPQKAARKPTAAAFISQQLQSLKSL-----T 217
QY 461 TISLTSPLALAVIRVNASSENTTFVVAQDPANLOVLSLETOAPENSIGTITLTPSSLMNNL 520
Db 218 SVSPLGDTLTFEEDRVNATVWKLPPTAGLEDLHHSQEEQSEVOAYLULLPRAVFOQT 277
QY 521 PAHDMELASVOEFNEFFETPALFQDPSLENLSLISVSSVANLTVRNLTNRNVTYTKHI 580
Db 278 RRRRDDAKRLVVDFFSQALFQDNSSQV-LGEKVLGIVQNTKVTNLSDPVLTFOH- 335
QY 581 NPSDELTVCVFW-DLGRNGRGWSDNGSCVKORRLNETICTCSHLTSFGVLLDLSRT 639
Db 336 QPQPKNTVLOCVFWVEDPASSTGSSWAGCETVSRD-TQTSLCNHLYFAVLM-VSST 393
QY 640 SVLPAQMMALFTIYICGLSIFLSVLTVAIEKIRRDYPSKILIOCAALLNLNV 699
Db 394 EVEATHKHYLLSVGCVISALACVFIIAYLCRRKSRDYTIKVMNLLSAVFLDVS 453
QY 700 FLDSWIALYKMGICISAVFVFLHYFLVLSFTWMGLEAFHMYLALVKVFNTYTKYILKF 759
Db 454 FLLSEPVALTGSEACRTSAMFLHFSLLAELSLWMLGEGYLNLYRVVEVFGTYVPGYLLKL 513
QY 760 CIVGWPVAVVVTIILTISPONG--LGSYGKFPNG-SPDDFCWINNNAVFIYTVVGYFC 816
Db 514 SIVGMPFVLTVALVDVNNYGPILAVRRTPERVTPSCWIRDSLSVYVTNLGLFS 573
QY 817 VIFLNVSMFTVWLVOLCRKKKOLGAORKTSTODLRSIAGLTFILGITWGAFFAW-- 874
Db 574 LVFLNLAFLATVWVQILRLPHSQ-----NPHVLTLLGLSLVGLPWALVFFSFAS 626
QY 875 GPVNVTFMYLFAINTLOGFFIFICYVAKENVRKOW--RRYLCCKGLRLAENSDWSKTA 932
Db 627 GTFQVLVLYLFSITSYQGLFLMW-----WSMRFOAQGGPSPKLNNSSDSAKL- 675
QY 933 TNLGKKQTVNOGVSSSS 949
Db 676 -----PISSGSTSSS 685

RESULT 5
Q05966 PRELIMINARY; PRT; 687 AA.
AC Q05966;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TM7XN1 PROTEIN PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99198960; PubMed=10100861;
RC Zelman A.J.W., Cornelissen I.M.H.A., Weidle U.H., Ruiter D.J.,
RA Van Muijen G.N.P.;
RT "TM7XN1, a novel human EGF-TM7 like protein, detected with mRNA
RT Differential display using human melanoma cell lines with different
RT metastatic potential.";
RL FEBS Lett. 446:292-298(1999).
DR EMBL; AJ011001; CAB37294.1; -.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF01825; GPS; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00303; GPS; 1.
DR PROSITE; PS00455; AMP_BINDING; UNKNOWN_1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 25 POTENTIAL.
FT CHAIN 26 687 TM7XN1 PROTEIN.

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SQ SEQUENCE 687 AA; 77150 MW; B3F0EE75B0CD5CF1 CRC64;

Query Match 11.8%; Score 629; DB 4; Length 687;
Best Local Similarity 28.4%; Pred. No. 7e-36;
Matches 177; Conservative 114; Mismatches 245; Indels 88; Gaps 19;

QY 360 PPVKAS-----FSSPTVSAPANVNTTSA--PPVQTDIVNTSSISDLENQVLOMEKALSIG 412
DB 133 PPLATSVTSWSPQNISLPSAASFTFSFSPHTAAHNASV-----DMCELKRDQL- 185
QY 413 SLEPNLAGEMINQVSRLLHSP-----DMLAPLAQRLKLVVDIGLQLNFSNTTISTSP 467
DB 186 -----LSQFLKHQKASRRPSAASQOQSLESKL-----TSVREMGD 224
QY 468 SLALAVIRVNASSNTTFFVAQDPANQVLSLETOAPENSIGTITLPSLSMNNLPAHDMEL 527
DB 225 MVSEEDIRINATVWKLOPTAGLQDLHIHSRQEEQSEIMEYSVLLPRTLFQRTKGRGEA 284
QY 528 ASRVQNFETPALFQDPSPLENLSISVISSVANLTVRNLTNRNVTTLKH-INPSQDE 586
DB 285 EKRLLLVDFSSQALFQDKNSSHV-LGEKVLGIVVQNTKVANLTPVVLTFQHQLOPK--N 341
QY 587 LTVRCVFW-DLGRNGRGWGSDNGSVKDRRLNETICTSHLTSFGVLLDLSRTSVLPQA 645
DB 342 VTLCQVFWEDPTLSSPGHWSAGCETV--RRETQTSFCNHLTYFAVLM--VSSVEVDVAVH 399
QY 646 MMALFTFTYICGGLSSIFLSVTLVTYIAFEKTRRDPSPSKILQICLCAALLNLVFLDLSW 705
DB 400 KHYLSLVYGCVCVVSALACLVTAIAYLCSSRKPRDYTIKVMNLLAVFLDTSFLLSEP 459
QY 706 ILYKKQGLCISVAVFLHYFLVFTWMLGFAFMYLALVKVFNTRYIRKYILKFCIVGWG 765
DB 460 VALTGEAGCRASAIHFHLSLLTCLSMGLEYNLYRLVVEFGTVPGVLLKSAMGWG 519
QY 766 VPAAVVTIILTSIDPNYG--LGSYCKPENG--SPDPCFWINNNNAVFIITVGYCVIFLLN 822
DB 520 FPIFLVTLVALVDVNTGPIILAVHRTPEGVTPSMCWIRDSLVSYITNLGFSLVFLFN 579
QY 823 VSMFIVVLVQLCKKKQKQAGKRTSTQDLRSIAGLTLGLITWGFAFFAW--GPNVNT 880
DB 580 MAMLATMVQILRLPHTQKWSH-----VLTLLGLSLVLGLPWLALIFESFASGTFQIV 632
QY 881 FMYLFAINTLOGFFIFCYCAKENVKQWRRLCCGKRLRAENSDWSKATNGLKKQT 940
DB 633 VLYLSIITSFQGLFIWIYW---SMRLQARG-----GPSPLKNSD----- 671
QY 941 VNOGVSSSSNSLQSSNSTNTTL 964
DB 672 -----SARLPISGSGTSSSRI 687

RESULT 6
Q96HB4 ID Q96HB4 PRELIMINARY; PRT; 693 AA.
AC Q96HB4:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE G-PROTEIN-COUPLED RECEPTOR 56.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA, AND CHORIOCARCINOMA;
RA Strausberg R.
RL Submitted (MAY 2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008770; AA08770.1; -
KW Receptor.
SQ SEQUENCE 693 AA; 77746 MW; 5C9FA8194D1B5C50 CRC64;

Query Match 11.5%; Score 618; DB 4; Length 693;
Best Local Similarity 28.1%; Pred. No. 4.2e-35;
Matches 177; Conservative 114; Mismatches 245; Indels 94; Gaps 20;

QY 360 PPVKAS-----FSSPTVSAPANVNTTSA--PPVQTDIVNTSSISDLENQVLOMEKALSIG 412
DB 133 PPLATSVTSWSPQNISLPSAASFTFSFSPHTAAHNASV-----DMCELKRDQL- 185
QY 413 SLEPNLAGEMINQVSRLLHSP-----DMLAPLAQRLKLVVDIGLQLNFSNTTISTSP 467
DB 186 -----LSQFLKHQKASRRPSAASQOQSLESKL-----TSVREMGD 224
QY 468 SLALAVIRVNASSNTTFFVAQDPANQVLSLETOAPENSIGTITLPSLSMNNLPAHDMEL 527
DB 225 MVSEEDIRINATVWKLOPTAGLQDLHIHSRQEEQSEIMEYSVLLPRTLFQRTKGRGEA 284
QY 528 ASRVQNFETPALFQDPSPLENLSISVISSVANLTVRNLTNRNVTTLKH-INPSQDE 586
DB 285 EKRLLLVDFSSQALFQDKNSSHV-LGEKVLGIVVQNTKVANLTPVVLTFQHQLOPK--N 341
QY 587 LTVRCVFW-DLGRNGRGWGSDNGSVKDRRLNETICTSHLTSFGVLLDLSRTSVLPQA 645
DB 342 VTLCQVFWEDPTLSSPGHWSAGCETV--RRETQTSFCNHLTYFAVLM--VSSVEVDVAVH 399
QY 646 MMALFTFTYICGGLSSIFLSVTLVTYIAFEKTRRDPSPSKILQICLCAALLNLV 699
DB 400 KHYLSLVYGCVCVVSALACLVTAIAYLCSSRKPRDYTIKVMNLLAVFLDTS 459
QY 700 FLDSWIALYKMQGLCISVAVFLHYFLVFTWMLGFAFMYLALVKVFNTRYIRKYILK 759
DB 460 FLLSEPVALTGEAGCRASAIHFHLSLLTCLSMGLEYNLYRLVVEFGTVPGVLLKL 519
QY 760 CIVGWGPVAVVTIILTSIDPNYG--LGSYCKPENG--SPDPCFWINNNNAVFIITVGYFC 816
DB 520 SAMGWGFPFLVTLVALVDVNTGPIILAVHRTPEGVTPSMCWIRDSLVSYITNLGLFS 579
QY 817 VIFLLNVSMFIVVLVQLCKKKQKQAGKRTSIQDLRSIAGLTLGLITWGFAFFAW-- 874
DB 580 LVFLFNWMLATMVQILRLPHTQKWSH-----VLTLLGLSLVLGLPWLALIFESFAS 632
QY 875 GPNVNTFMYLFAINTLOGFFIFCYCAKENVKQWRRLCCGKRLRAENSDWSKATN 934
DB 633 GTFQLVLYLSIITSFQGLFIWIYW---SMRLQARG-----GPSPLKNSD----- 677
QY 935 GLKKQTVNQGVSSSSNSLQSSNSTNTTL 964
DB 678 -----SARLPISGSGTSSSRI 693

RESULT 7
Q9Y653 ID Q9Y653 PRELIMINARY; PRT; 693 AA.
AC Q9Y653:
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE G-PROTEIN-COUPLED RECEPTOR.
GN GPR56.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99168899; PubMed=10049584;
RA Liu M., Parker R.M., Darby K., Eyre H.J., Copeland N.G., Crawford J.,
RA Gilbert D.J., Sutherland G.R., Jenkins N.A., Herzog H.;
RT "GPR56, a novel secretin-like human G-protein-coupled receptor gene.";
RL Genomics 55:296-305(1999).
DR EMBL; AF106858; AAD30545.1; -
DR InterPro; IPR000873; AMP-blind.
DR InterPro; IPR000832; GPCR_secretin.

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DR InterPro: IPR000203; PKD_cys_rich.
DR Pfam: PF000002; 7tm_2; 1.
DR PRINTS: PF01825; GPS; 1.
DR SMART: SM00303; GPS; 1.
DR PROSITE: PS00455; AMP_BINDING; UNKNOWN.1.
DR PROSITE: PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 693 AA; 77753 MW; F71C8E62666A5141 CRC64;

Query Match 11.5%; Score 617.5; DB 4; Length 693;
Best Local Similarity 28.3%; Pred. No. 4.6e-35;
Matches 174; Conservative 115; Mismatches 245; Indels 81; Gaps 20;

360 PPVKAS-----FSSPTVSAPANVNTSA--PPVQTDIVNTSISDLENQVLOMEKALSIG 412
Db 133 PPLATSVTSWSPONISLSPASAFTHSPHPPHAAHNSV-----DMCELRDLQL- 185
QY 413 SLEPNLAGEMINQVSRLLHSP-----DMLAPLAQRLKLVVDDIGLQNFSTTISLTP 467
Db 186 -----LSQFLKHPQKASRRPSAASOOLQLESKL-----TSVRFMGD 224
QY 468 SLALAVIRVNASSENTTTFVAQDPANQVLSLETPAQENSIGITTLPSLSMNNLPAHDMEL 527
Db 225 MVSEEDRINATVWKLOPTAGLQDLHIHSRQEEQSEIMEYSVLLPRTLQRTKGRGEA 284
QY 528 ASRVQNFETPALFQDPSLENLSISVISSVANLTVRNLTNRVTVLKH-INSQDE 586
Db 285 EKRLLLVDFSSQALFQDKNSQV-LGEKVLGVVQNTKVANLPEPVLTFFQHQLOPK-N 341
QY 587 LTVRCVFW-DLGRNGRGWSDNGCSVKDRRLNETICTCSHLTSFGVLLDLSRTSVLPAQ 645
Db 342 VLOCVFWEDPTLSSPGHWSAGGETV-RRETQSCFCNHLTYFAVLM-VSSVEVDVH 399
QY 646 MMALTFITYICGLSSIFLSVLTLYIA-----FKIRRDYPSKILIOCAALLLNLY 699
Db 400 KHYLSLLSYGVGWSALACLVTAAYLCSRVPLPCRRKPRDYTIKVMNLLAVFLDTS 459
QY 700 FLDSWIALYKMOGLCISAVPLHFLVLSFTWGLAEFHYLALVKVFNTRYKYLKE 759
Db 460 FLLSEPVALTSEACRASAIPLHSLTCLSMWGLEGNLYRLVVEVFTYVPGYLLKL 519
QY 760 CIVGNGVPAVVVITILISPNDYG--LGSYGFPNG-SPDDFCWINNNNAVYITVGYFC 816
Db 520 SAMGNGFFIFLTVLALVDVNGYPIILAVHRTPEGVIVPSMCWIRDSLYITNLGLFS 579
QY 817 VIFLNVSMFIVVLVOLCRKKKQGLGAOKRTSIQDLRSTAGTLFLLGITWGAFFAW-- 874
Db 580 LVFLFNMAMLATMVVQILRLPHTQKWSH-----VLTLLGLSLVLGLPWAFLFFSFAS 632
QY 875 GPVNVTFMYLFAIFNTLQGGFFIFCYKAKENVKQWRRYLCCKGLRLAENSDWKTATN 934
Db 633 GTFQLVLYLFLSITTSFQGLFIYFW-----SMRLQARG-----GPSLKNSDCARL---- 681
QY 935 GLKKTQVNGVSSSS 949
Db 682 -----PISGGTSSS 691

RESULT 8
Q9UHX3 PRELIMINARY; PRT; 823 AA.
AC Q9UHX3.
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE EGF-LIKE MODULE EMR2.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;

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RN SEQUENCE FROM N.A.
RP MEDLINE-20366136; PubMed=10903844;
RA Lin H.-H., Stacey M., Hamann J., Gordon S., McKnight A.J.;
RT "Human EMR2, a novel EGF-TM7 molecule on chromosome 19p13.1, is
RT closely related to CD97.";
RL Genomics 67:188-200(2000).
DR EMBL: AF114491; AAF21974.1; -.
DR HSPSP; P16109; IFSB.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR000832; GPCR_secretin.
DR InterPro: IPR000203; PKD_cys_rich.
DR Pfam: PF000002; 7tm_2; 1.
DR Pfam: PF000008; EGF; 2.
DR Pfam: PF01825; GPS; 1.
DR PRINTS: PR00249; GPCRSECRETIN.
DR SMART: SM00179; EGF_CA; 4.
DR SMART: SM00303; GPS; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS01187; EGF_CA; 4.
DR PROSITE: PS0261; G_PROTEIN_RECEP_F2_4; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
KW SEQUENCE 823 AA; 90505 MW; ID9FA9AAA0D90553 CRC64;

Query Match 11.0%; Score 589; DB 4; Length 823;
Best Local Similarity 27.3%; Pred. No. 5.9e-33;
Matches 247; Conservative 120; Mismatches 327; Indels 212; Gaps 46;

QY 158 PQNHITNGTL-----TGVLSLSLKRS-----ELNK--TLQILSETYFIMCATAEAGST 205
Db 34 PODSSCVNATACRCNPGFSFSEIITTPMETCDIDINECATILSKVSCGKFCDCWTEGYSYD 93
QY 206 LNCIT-----FTIKLNTNMNACAII-----AALERVK 231
Db 94 CVCSPGYEPVSGAKTFK-NESENTQDQVDECCQNPRLCKSYGTCVNLGYSYTCQCLPGFK 152
QY 232 IRPME-----HCCSCVRIPCSPSP---BELGKLOCDLQDPIVCLADHPHPPFPSSQS 281
Db 153 LKPEDPKLCTDYNECTSGQNPCHSSTHCLNNVSGYQCR-----PGWQPIPGS-- 201
QY 282 IPVPRATVLSQVPKATSAEPDPYSPVTHN-VSPGTEIQP-LSPQPSAPIASSPAIDM 339
Db 202 -PNGPNNTVCEDVDECSGQHCQDSSTVCFTVGSYSCRCRPGMKPRHGP- 251
QY 340 PQSETISSPMPTQVSGTPPVKASFSPTVSAPANVNTTSAPPVQTDIVNTSISDLE 399
Db 252 NNQKDTVCEDM--TFSTWTPPP-----GVH 274
QY 400 NOVLO--MEKALSIG-SLEPNLAGEMINQV-----SRLHSPDM-LAP-----LAQRLL 445
Db 275 SQTLSRFFDKVQDLGRDYKPLGANNITIQSILQALDELLEAPGDLTLPRLQOHCVASHL 334
QY 446 KVDDI--GLQNFSTTISLTPS---LALAVIRVNASSENTTTFVAQDPANQVLSLET 500
Db 335 DGLVDVLRGLSKNLNGLNFSYPAGTELSLEV---QKQVDRSVTLRQNAVMQMDW-N 389
QY 501 QAPENS-----IGTITLPSLSMNNLPAH-DMELASRVQENFFET-PALFQDPSLENLSL 552
Db 390 QAKSGDGPSPVGLVSIIPG--MGKLLAEAPLVLEPEKQMLLHETHOGLLODGS---PIL 444
QY 553 ISYVISSVANLTVRNLTNRVTVLKH--INPSODELTVCVFWDLGNRGGRGSDNCC 610
Db 445 LSDVISAFLSNNDTNLSPPVTFTHSRSVTPRQ---KVLGVFWHEGQN-GCGHWATTGC 500
QY 611 SVKDRRLNETICTCSHLTSFGVLL---DLSTSVLPQAQMMALTFITYICGGLSSIFLSVT 667
Db 501 STTGTRDTSTICRCHTLSSFAVLMAHYDQVEDPV-----LTVITYMGLSVSLCLLIA 554
QY 668 LVTYIAFEKIRRDYPSKILIOCAALLLNLYFLDLSWIALYKMOGLCISAVFLHYFL 727

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QY 763 GNGVPAVVTIITISPDNVTGLSGYKFPNGSPDDFCWNNNAVYITVVGFCVIFLLN 822
Db 944 GYLFPATVVGSAIDYKSYG-----TEKACWLHVDNYFWSFIGFVPTFIILLN 992
QY 823 VSMFIVVLQCLRIKKKQOLGAOKTTSIQDLRS-IAG-----LTFLLGITWGAFFAWGPVN 878
Db 993 I---IFLVITLCRWKHSNLTLPDSSSLENIKSVLGAFCALLCLLGLTWSGGLLFINET 1049
QY 879 VTPMYLFAINTLQGFIFIFCYCAKENVRKQW-----RRYLCCGKL----- 920
Db 1050 IVMAYLFTIENAGQVFIFIFHCALQKKVRKEYCKCFRHSYCCGGLPTESPSSVKAST 1109
QY 921 -RLAENSWSKATNGLKQTVNGCVSSSSSLOSSTNSTTLLVNDSCSVHAGS--- 976
Db 1110 RTSARYSSGTSQSRIRRMWMDTVKQSESSFTSGDINSTLNGHSLNARDTSAMDITLP 1169
QY 977 -NGNASTERNGVSFSVQNGD 995
Db 1170 LNCNFNN-----SVSLHKG 1184
RESULT 10
O97823 PRELIMINARY; PRT; 1283 AA.
ID O97823
AC O97823
DT 01-MAY-1999 (TREMREL. 10, Created)
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)
DT 01-OCT-2001 (TREMREL. 18, Last annotation update)
DE LATROPHILIN 3 SPLICE VARIANT ABBH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148828; PubMed=10025961;
RA Matsushita H., Lellanova V.G., Ushkaryov Y.A.;
RT "The latrophilin family: multiply spliced G protein-coupled receptors
with differential tissue distribution.";
RL FEBS Lett. 443:348-352(1999).
DR EMBL; AF11090; AAD05326.1; .
DR InterPro; IPR000922; Gal_Lectin.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormo_receptor.
DR InterPro; IPR003334; Latrophilin.
DR InterPro; IPR003112; Olfac_like.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02140; Gal_Lectin; 1.
DR Pfam; PF01825; GPS; 1.
DR Pfam; PF02793; HRM; 1.
DR Pfam; PF02354; Latrophilin; 1.
DR Pfam; PF02191; OLF; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRODOM; PD005612; Gal_Lectin; 1.
DR SMART; SM00303; GPS; 1.
DR SMART; SM00008; Hormr; 1.
DR SMART; SM00284; OLF; 1.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS50228; SUEL_LECTIN; 1.
SQ SEQUENCE 1283 AA; 143897 MW; 9D87F15DD6D01EC0 CRC64;
Query Match 10.0%; Score 536.5; DB 6; Length 1283;
Best Local Similarity 23.7%; Pred. No. 5.3e-29;
Matches 206; Conservative 124; Mismatches 334; Indels 205; Gaps 30;
QY 260 LQDPTVCLADHPRGPPFSSSQSIPVVRATVLSQVPKATSFAPDPDYPVTHNVPSPIGE 319
Db 409 ISPPHLSDLERPPVREISTTGTGLTGTSTTTTLRTTT-----WSPGRSTTPSVSGR 462

QY 320 IQPLSPOPSAPIASSPAIDMPPQSETISSPMPQTHVSPPTPPVKASFSS----- 368
Db 463 RNKSTSP-----SPAELVNDI-----TTHVPSASPOIPALEESCEAVEAREIMW 508
QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSISDLENQVLOMEKALS 410
Db 509 FKTRQGMQAPCPAGTIGVSTYLCAPDGIWDGPGDPLSNCS--SPWVNHITQKLKS--- 564
QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440
Db 565 -GETAANIARELAETRNHLNAGDTITYSVRAMDQLVGLLDVQLRNLTPGKDSAAARSLNK 623
QY 441 -----AQRLLKVYDDIGLQNFN-----TTISLSPSLALAVIR-----VNAS 479
Db 624 LQKRESCRAYVQAMVETVNNL-LQPQALNAWRDLTTSQDLRAATMLLDVVEESAFVLAD 682
QY 480 SFNTTTFVAQDPANLOVSLETOAPENSIGTITLPSSL-----MNNLPAMDMLASR 530
Db 683 NLLKTDIVRENTDNTQLEVARLSTEGNLEDLKFPENTGHCSTIQLSANTLUKQNRNGEIR 742
QY 531 VOENFFET--PALFODPSLENLSL-----ISYVISSSVANLTVRN-----LTR 571
Db 743 VAFVLYNNLGPYL-----STENASMKLGTAMSTNHSVIVNSPVITAAINKEFSNKVYLAD 798
QY 572 NVTYTLKHINPSQDELTVCVFWDLGRNGRGWDSNGSVKDRRLNETICTCSHLTSFG 631
Db 799 PVFTVKHIKQSEENFNPCSFWSYKRTMTGYWSTQGGRLTNTKTHHTTCSNHLTNFA 858
QY 632 VLL---DLSRTSVLPAQMMALFTIYIGGLSIFLSTVLTVIAFEKIRRDYPSKILIQ 688
Db 859 VLMARVVKHSDAV--HDLDDVITWVGILLSLVCLLICIFTCFPGQLQSD-RNTIHN 915
QY 689 LCAALLNLNLFLL-----DSWIALYKMOGLCISAVFVLFYLLVSTWGLFAFHMYLA 743
Db 916 LCISLFAELLFLIGINRTDQPIA-----CAVFAALLHFFFLAFTWMLFEGVQLYIM 968
QY 744 LVKVENT--YIRKYILKFCVIGWGPVAVVVTIILTISPDNVLGSGYKFPNGSPDDFCWI 801
Db 969 LVEFPESEHSRKY---FYLGVGMPALIVAVSAADYRSYG-----TDDKVCWL 1014
QY 802 NNAVYITVVGFCVIFLLNVSMFIVVLVQLCRIKK--KKQLGAOKRTSIQDLR----- 854
Db 1015 RLDYTFIWSFIGPATLIIMLVIFGLIYALYKMFHHTAILKPESGLDNINVEDNRPEIKS 1074
QY 855 ---STAGTLFLGITWGAFFAWGPVNVTVMYLPALTNTLQGFIFIFCYCAKENVRKQW 911
Db 1075 WVIGAIALLCLLGLTWAFGLMYNESTVIMAYLFTIFNSLQGMFIFIFHCVLQKKVRKEY 1134
QY 912 RRYL--CC-----GKRLAENSWSKATNGLKQTVNGCVSSS 948
Db 1135 GKLRTHCCSGRSTESSIGSGKTSGRTPGRTYSGSRIRRMWMDTVKQSESSFTIGD 1194
QY 949 SNSLOSSTNSTTLLVNDSCSVHAGSN 977
Db 1195 INSSASLNRGAMNHLISNALLRPHGTNN 1223
RESULT 11
O97829 PRELIMINARY; PRT; 1351 AA.
ID O97829
AC O97829
DT 01-MAY-1999 (TREMREL. 10, Created)
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE LATROPHILIN 3 SPLICE VARIANT BBH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148828; PubMed=10025961;

RA Matsushita H., Lelianova V.G., Ushkaryov Y.A.;
 RT "The latrophilin family: multiply spliced G protein-coupled receptors
 RL FEBS Lett. 443:348-352(1999).
 DR EMBL: AF111096; AD05332.1;
 DR InterPro: IPR000922; Gal_lectin.
 DR InterPro: IPR000832; GPCR_secretin.
 DR InterPro: IPR001879; hormn_receptor.
 DR InterPro: IPR003334; Latrophilin.
 DR InterPro: IPR003112; Olfac_like.
 DR InterPro: IPR000203; PKD_cys_rich.
 DR Pfam: PF00002; 7tm_2; 1.
 DR Pfam: PF02140; Gal_lectin; 1.
 DR Pfam: PF01825; GPS; 1.
 DR Pfam: PF02793; HRM; 1.
 DR Pfam: PF02354; Latrophilin; 1.
 DR Pfam: PF02191; OLF; 1.
 DR PRINTS: PR00249; GPCRSECRETIN.
 DR PRODOM: PD005612; Gal_lectin; 1.
 DR SMART: SM00303; GPS; 1.
 DR SMART: SM00008; Hormr; 1.
 DR SMART: SM00284; OLF; 1.
 DR PROSITE: PS50227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE: PS50261; G_PROTEIN_RECEP_F2_4; 1.
 DR PROSITE: PS50228; SUEL_LECTIN; 1.
 DR SEQUENCE 1351 AA; 150807 MW; 7C085DE9224C742A CRC64;

Query Match 10.0%; Score 536.5; DB 6; Length 1351;
 Best Local Similarity 23.7%; Pred. No. 5,7e-29;
 Matches 206; Conservative 124; Mismatches 334; Indels 205; Gaps 30;

QY 260 LQDPIVCLADHPRGPPFSSQSIPVVPVATVLSQVPKATFAEPDPYSPVTHNVPSPIGE 319
 DB 477 ISPPHILDSLDLPPVREISTTGLTGTSTTTTLRTTT-----WSPGRSTTPSVGR 530

QY 320 IQPLSPQPSAPIASSPAIDMPQSETISSPMPQTHVSGTPPPVKASFSS----- 368
 DB 531 RNRISSTP-----SPAIEVLNDI-----THVPSASQIIPALESCAEAREINMW 576

QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSISDLENQVLMKEKALS 410
 DB 577 FKTRQGMKQPCPAGTIGVSTYLCIAPDGIWDPGQDLSNCS--SPWNHITQKLKS-- 632

QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPQMLAPL----- 440
 DB 633 -GETAANTARELAETRNHLNAGDIYSVRAMDQVLGLLDVQLRNLTPGGKDSAARSLNK 691

QY 441 -----AQLKLVDDIGLQLNFSN-----TTISLTSPSLALAVIR-----VNAS 479
 DB 692 LQKRERSRAYVQAMVETVNNL-LQPOALNAWRDLTTSQDLRAATMLLDVTEESAFVLAD 750

QY 480 SFNTTTFVAQDPANLQVLSLETQAPENSIGTITLPSSL-----MNNLPAHDMELASR 530
 DB 751 NLLKTDIVRENDIIOLEVARISLTCGNLEDLKPFGTNGHSTIQLSANTLKQNGRGEIR 810

QY 531 VQNFET--PALFQDPSLENLSL-----ISYVSSVANLATVRN-----LTR 571
 DB 811 VAFVLYNNGPYL-----STENASMKLGTEAMSTNHSIVNSPVITAINKEFSNKVYLAD 866

QY 572 NVTYTLKHINFSQDELTVRCVFDWLGNGRGWSNCGSVKORRLNETICTCSHLTSFG 631
 DB 867 PVVFTVHKIKOSENENFNCSEFSWSYKRTMTGYWSTQGCRLTLTKTKTSCNHLTNFA 926

QY 632 VLL---DLRSTSVLPQAOMALFFITYIGCGLSIFLSVLTVTYIAFEKIRRDYFSKILIQ 688
 DB 927 VLMHAEVVKHSDAV--HDLLEDVITWIGLLSVLCLICITFTCFFFRGLOSD-RNTIHN 983

QY 689 LCAALLNLNVLFL-----DSWIALYKMGCLCISAVFLHYFLVLSFTWMLGLEAFHMYLA 743
 DB 984 LCISLFAELFLIGINTDQPIA-----CAVFAALLHFFFLAFAFTWFLQVQLYIM 1036

QY 744 LVKFVNT--YTRKYLKFCVIGWGVPAVVVITILTISPQNYGLGSYGKFPNGSPDPCFWI 801

DB 1037 LVEFESEHSRRKY---PYLVGYGMPALIVAVSAADYRSYG-----TDKVCWL 1082
 QY 802 NNAVFYITVVGVCVIFLLNVSMFIVVLVOLCRICK--KKOLGAQRKTSIOTDLR----- 854
 DB 1083 RLDTYFTWFSFGPATLIIMLVNFIAGIALYKMFHTAILKPESGCLDNIYEDNRPFIKS 1142
 QY 855 ---SIAGLTFLGITMGFAFFAWGPNVNTFMVYFAIFNTLQGFIFIFYCVAKENVRKQW 911
 DB 1143 WVIGATALLCLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFHCVLQKKVKEY 1202
 QY 912 RRYL---CC-----GKRLAENSWSKTATNGLKKQTWQGVSSS 948
 DB 1203 GKCLRHCCSGRSTESSIGSOKTSGSRTPGRYSTGQSQRIRRMWNTVVRKQSSSFTGD 1262
 QY 949 SNSLQSSNSTNTLLVNDNCDSVHASGN 977
 DB 1263 INSSASINRGAMANHLITSNALLRPHGTNN-1291

RESULT 12
 Q97821 PRELIMINARY; PRT; 1512 AA.
 ID O97821
 AC O97821;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
 DE LATROPHILIN 3 SPLICE VARIANT ABBF.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_taxid=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99148928; PubMed=10025961;
 RA Matsushita H., Lelianova V.G., Ushkaryov Y.A.;
 RT "The latrophilin family: multiply spliced G protein-coupled receptors
 RT with differential tissue distribution."
 RL FEBS Lett. 443:348-352(1999).
 DR EMBL: AF111098; AD05324.1;
 DR InterPro: IPR000922; Gal_lectin.
 DR InterPro: IPR000832; GPCR_secretin.
 DR InterPro: IPR001879; hormn_receptor.
 DR InterPro: IPR003334; Latrophilin.
 DR InterPro: IPR003112; Olfac_like.
 DR InterPro: IPR000203; PKD_cys_rich.
 DR Pfam: PF00002; 7tm_2; 1.
 DR Pfam: PF02140; Gal_lectin; 1.
 DR Pfam: PF01825; GPS; 1.
 DR Pfam: PF02793; HRM; 1.
 DR Pfam: PF02354; Latrophilin; 1.
 DR Pfam: PF02191; OLF; 1.
 DR PRINTS: PR00249; GPCRSECRETIN.
 DR PRODOM: PD005612; Gal_lectin; 1.
 DR SMART: SM00303; GPS; 1.
 DR SMART: SM00008; Hormr; 1.
 DR SMART: SM00284; OLF; 1.
 DR PROSITE: PS50227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE: PS50261; G_PROTEIN_RECEP_F2_4; 1.
 DR PROSITE: PS50228; SUEL_LECTIN; 1.
 DR SEQUENCE 1512 AA; 169140 MW; 792CDD8790C4AA9B CRC64;

Query Match 10.0%; Score 536.5; DB 6; Length 1512;
 Best Local Similarity 23.7%; Pred. No. 6,6e-29;
 Matches 206; Conservative 124; Mismatches 334; Indels 205; Gaps 30;

QY 260 LQDPIVCLADHPRGPPFSSQSIPVVPVATVLSQVPKATFAEPDPYSPVTHNVPSPIGE 319
 DB 409 ISPPHILDSLDLPPVREISTTGLTGTSTTTTLRTTT-----WSPGRSTTPSVGR 462

QY 320 IQPLSPQPSAPIASSPAIDMPQSETISSPMPQTHVSGTPPPVKASFSS----- 368

Thu May 23 07:45:03 2002

RT	RT	"The latrophilin family: multiply spliced G protein-coupled receptors with differential tissue distribution."	
RL	FEBS Lett. 443:348-352(1999).		
DR	EMBL: AF111094; AAD05330.1; .		
DR	InterPro: IPR000922; Gal_lectin.		
DR	InterPro: IPR000932; GPCR_secretin.		
DR	InterPro: IPR001879; hormn_receptor.		
DR	InterPro: IPR003334; Latrophilin.		
DR	InterPro: IPR003112; Olfac_like.		
DR	InterPro: IPR002033; PKD_cys_rich.		
DR	Pfam: PF00002; 7tm_2; 1.		
DR	Pfam: PF02140; Gal_lectin; 1.		
DR	Pfam: PF01825; GPS; 1.		
DR	Pfam: PF02793; HRM; 1.		
DR	Pfam: PF02354; Latrophilin; 1.		
DR	Pfam: PF02191; OLF; 1.		
DR	PRINTS: PR00249; GPCRSECRETIN.		
DR	ProDom: PD005612; Gal_lectin; 1.		
DR	SMART: SM00303; GPS; 1.		
DR	SMART: SM00008; Hormr; 1.		
DR	SMART: SM00284; OLF; 1.		
DR	PROSITE: PS50227; G_PROTEIN_RECP_F2_3; 1.		
DR	PROSITE: PS50261; G_PROTEIN_RECP_F2_4; 1.		
DR	PROSITE: PS50228; SUEL_LECTIN; 1.		
DR	SEQUENCE 1580 AA; 176050 MW; D527CBF4B937DA8D CRC64;		
QY	Query Match	10.0%; Score 536.5; DB 6; Length 1580;	
DB	Best Local Similarity	23.7%; Pred. No. 7.1e-29;	
DB	Matches	206; Conservative 124; Mismatches 334; Indels 205; Gaps	
QY	260	LQDP IVCLADHPGPPFSSQSIPVVPRA TVLSQVPKATSPAEPPDYSVPVTHNPSPIGE	319
DB	477	ISPEIHLSDSLERPPVREISTGTLGTSITTTTLRTTT-----WSPGRSTTPSVSGR	530
QY	320	IQPLSOPSPAPIASSPAIDMPPQSETISSPMPQTHSVGTPPVKASPESS-----	368
DB	531	RNRSTSTP-----SPAELVNDI-----THVPSASQIIPALESCAEAREIMW	576
QY	369	-----PTVSAPANVNT--TSAP-----PVQTDIVNTSSISDLENOVLQMEKALS	410
DB	577	FKTRQGQMAKQPCPAGTIGVSTYLC LAPDGIWD PQGPDLNCS--SPWVNHITQKLK--	632
QY	411	LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL-----	440
DB	633	-GETAANIARELAEOCTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGKDSAARS LNK	691
QY	441	-----AQRLLKVDDIGLQLNFSN-----TTISLTSPLALAVIR-----VNAS	479
DB	692	LQKRSCRAYQAVQAVETVNNL-LQPQALNAWRDLTTSQDLRAATMLDITVEESAFVLAD	750
QY	480	SNFTTTFVAQDPANLQVLSLETOAPENSIGTITLPSSL-----MNNLPAHDMELASR	530
DB	751	NLLKTDIVRENTDNIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKGNGRGEIR	810
QY	531	VOENFFET--PALFQDPSPLENLSL-----ISYVISSVANLTVRN-----LTR	571
DB	811	VAFVLYNNLGPYL-----STENASMKLGTEAMSTNHSVIVNSPVITAAINKEFSNKVYLAD	866
QY	572	NVTVTLKHIINFSODELTVCRCVFDWLCGRNGRGWSDNGSKVDRLNETICTCSHLTSEF	631
DB	867	PVFTVKHKIKOSEENFNPCSEFSYKRTMTGYWSTQCGRLTTTKHTTCSNHLTNFA	926
QY	632	VLL---DLSRTSVLPAQMALTFTIYIGCGLSSIFLSVTLVTIYIAFEKIRRDYPSKILIQ	688
DB	927	VLMAHVEVKHSDAV--HDLLEDVITWVGILLSLVCLLICITFCFFRGLQSD--RNTIHN	983
QY	689	LCAALLNLLNLFLL-----DSWIALYKMQGLCISVAVFLHYLLYSFTWGLAEAPHWILA	743
DB	984	LCISLFAELLFLIGINRTDQPIA-----CAVFAALLHFFFLAFTWMFLEGVOLYIM	1036
QY	744	LVKVENT--YIRKYILKFCIVGWGPVAVVVTIILITSPDNYGLSGYKFPNGSPDPFCWI	801


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Db 694 RERSCRAYQAVMETVNNL-LQPQALNAWRDLTTSQDLRAATMLLDTVEESAFVLADNLL 752
QY 483 TTTTFVAQDPANLQVSLQTPENSIGTITLPSL-----MNNLPAHDMELASRVQF 533
Db 753 KTDIVRENTDNIQLEVARLSTEGNLEDKFPENTGHSTIOLSANTLQKONGRNGEIRVAF 812
QY 534 NFET--PALFQDPSENL--ISVVISSVANLTVRN-----LTVNVT 574
Db 813 VLYNNLGPYL-----STENASMKLGTEAMSTNHSVIVNSPVITAINKEFSNKVYLADPV 868
QY 575 VTLKHINPQDELTVRCVFDLGRNGRGWSDGSCVSKDRRLNETICTCSHLTSGVLL 634
Db 869 FIVKHIKQSEENFNPCSFWSYKRTMTGYSTQGCRLLTNTKTHTCSCNHLTNFAVLM 928
QY 635 ----DLRSTSVLPQAMALFTIYIGCGLSIFSLVTLVYIAFEKIRDYPSKILLIQLCA 691
Db 929 AHVEVKSDAV--HDLLEDVITWGIILSLVCLLICITFCFFRGLQSD-RNTIHKNLCI 985
QY 692 ALILLNLVFL-----DSWIALYKMQGLCISVAVFLHYFLVSVTWMLGFAFMYLALVK 746
Db 986 SLFVAELFLIGINRTDPTA-----CAVFAALLHFFFLAAFTWMLFEGVQLYIMLVE 1038
QY 747 VENT--YIRKYILKFCIVGVAVVVTIILITISPDNVLGSGYKFPNGSPDDFCWNN 804
Db 1039 VFESEHSRRKY---FVLVGYGMPALIVAVSAADVRSYG-----TDKVCWLRLD 1084
QY 805 AFVYITVGVFCVIFLLNVSMFIVVLVQLCRIKK--KKQLGAQRKTSIODLRSIAGLTFL 862
Db 1085 TYFIWFGIPGATLIIMLVIFLGLYALYKMFHTAILKPESCLONIKSWVIGAI--LCL 1143
QY 863 LGITWGAFFAFWGPVNVTFMFLAIFNTLQGFIFIFYCAKENVRKQW---RRYLCCG 918
Db 1144 LGITWAGLWYNINVESTVIMAYLFTIFNSLQGMFIFPHCVLQKVKRYGKCLRTHCCSG 1203
QY 919 KL-----RLAENS-----WSKATNGLKKQTQVNGVSSSSNSLQSS 955
Db 1204 KSPSSIGSGKTSGRTPGYSQSRIRRMWNT-----VRKOSSESFITGDIN-----S 1255
QY 956 SNTNSTTLVN--NDCSVHAS--GNGNASTERNRGVSFVQNGD 995
Db 1256 SASLREGLNARDTSVMDTLPNGN-----HGNSYSIAGGE 1293

RESULT 15
O97820 PRELIMINARY; PRT; 1274 AA.
AC O97820;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE LATROPHILIN 3 SPLICED VARIANT ABAB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148828; PubMed=10025961;
RA Matsushita H., Lelianaova V.G., Ushkaryov Y.A.;
RT "The latrophilin family: multiply spliced G protein-coupled receptors
RL with differential tissue distribution.";
RL FEBS Lett. 443:348-352(1999).
DR EMBL; AF111087; AAD05323.1;
DR InterPro; IPR000922; Gal.lectin.
DR InterPro; IPR000832; GPCR-secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR003334; latrophilin.
DR InterPro; IPR003112; olfac_like.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02140; Gal.lectin; 1.
DR Pfam; PF01825; GPS; 1.

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DR Pfam; PF02793; HRM; 1.
DR Pfam; PF02354; Latrophilin; 1.
DR Pfam; PF02191; OLF; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRODOM; PD005612; Gal_lectin; 1.
DR SMART; SM00303; GPS; 1.
DR SMART; SM00008; Hofmr; 1.
DR SMART; SM00284; OLF; 1.
DR PROSITE; PS02027; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS02061; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS0228; SUEL_LECTIN; 1.
SQ SEQUENCE 1274 AA; 142748 MW; 147C1B5FC160037F CRC64;

Query Match 10.0%; Score 534; DB 6; Length 1274;
Best Local Similarity 23.9%; Pred. No. 7, 9e-29;
Matches 206; Conservative 124; Mismatches 333; Indels 198; Gaps 30;

QY 260 LQDFIVCLADHPGPPFFSSQSIPIVPRATVLSQVPKATSAFAPDPDYSPTVTHNVPSPIGE 319
Db 409 ISPIHLSDSLERPPVREISTTGLTGTSTTTTLRTTT-----WSPGRSTTPSVSGR 462
QY 320 IQPLSPQSPAPIASSPALDMPQSETISSPMPOTHVSGTPPVKASFSS----- 368
Db 463 RNRSTSTP-----SPALEVLNDI-----TTHVPSASPOIPALEESCEAVEAREIMW 508
QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSISDLENQVLMQEKALS 410
Db 509 FKTRQGMQAKQPCAGTIGVSTYLCIAPDGIWDPOGPDLSNCS--SPWVNHITQKLKS-- 564
QY 411 LGSLEPNLAGMINOVSLHNS-----PDMLAPL----- 440
Db 565 -GETAANIARELAEQTRNHLNAGDITYSVRAMDQLVGLDVLQRLNLTGPGKDSAARSLNK 623
QY 441 -----AQLKKVVDIGIQLNFSN-----TTISLSPSLALAVIR---VNAS 479
Db 624 LQKERSGRAVQAWVEVNNL-LQPQALNAWRDLTTSQDLRAATMLLDTVESAFVLAD 682
QY 480 SNTNSTTLVN--NDCSVHAS--GNGNASTERNRGVSFVQNGD 995
Db 683 NLLKTDIVRENTDNIQLEVARLSTEGNLEDKFPENTGHSTIOLSANTLQKONGRNGEIR 742
QY 531 VQNFET--PALFQDPSENL--ISVVISSVANLTVRN-----LTVNVT 571
Db 743 VAFVLYNNLGPYL-----STENASMKLGTEAMSTNHSVIVNSPVITAINKEFSNKVYLAD 798
QY 572 NVTVTLKHINPQDELTVRCVFDLGRNGRGWSDGSCVSKDRRLNETICTCSHLTSGF 631
Db 799 PVFTVVKHIKQSEENFNPCSFWSYKRTMTGYSTQGCRLLTNTKTHTCSCNHLTNFA 858
QY 632 VLL---DLRSTSVLPQAMALFTIYIGCGLSIFSLVTLVYIAFEKIRDYPSKILLIQL 688
Db 859 VLMAHVEVKHSDAV--HDLLEDVITWGIILSLVCLLICITFCFFRGLQSD-RNTIHKN 915
QY 689 LCAALLNLVFL-----DSWIALYKMQGLCISVAVFLHYFLVSVTWMLGFAFMYLA 743
Db 916 LCISLFAELFLIGINRTDPTA-----CAVFAALLHFFFLAAFTWMLFEGVQLYIM 968
QY 744 LKVFENT--YIRKYILKFCIVGVAVVVTIILITISPDNVLGSGYKFPNGSPDDFCWI 801
Db 969 LVEVFESHSRRKY---FVLVGYGMPALIVAVSAADVRSYG-----TDKVCWLR 1014
QY 802 NNAVFYITVGVFCVIFLLNVSMFIVVLVQLCRIKK--KKQLGAQRKTSIODLRSIAGL 859
Db 1015 RLDTYFIWFSFIGPATLIIMLVIFLGLYALYKMFHTAILKPESCLDNITKSWVIGAI--L 1073
QY 860 TFLGITWGAFFAFWGPVNVTFMFLAIFNTLQGFIFIFYCAKENVRKQWRYL---C 916
Db 1074 LCLLGLTWAGLWYNINVESTVIMAYLFTIFNSLQGMFIFPHCVLQKVKRYGKCLRTHC 1133
QY 917 C-----GKRLAENSWSKATNGLKKQTQVNGVSSSSNSLQSS 956
Db 1134 CSGRSTESSIGSGKTSGRTPGYSQSRIRRMWNTVRKOSSESFITGDINSSASLN 1193

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Query Match 10.0%; Score 534; DB 6; Length 1503;
Best Local Similarity 23.9%; Pred. NO. 9.9e-29;
Matches 206; Conservative 124; Mismatches 333; Indels 198; Gaps 30;

260 LQDPVCLADHPRGPPFFSSQSIPVVPRATVLVSQVPKATSFPAEPDPSVPTHTNVPISGE 319
: || : | : | : | : | : | : | : | : |

Db 409 ISPIHLDSDLRPPVREISTGTGTLGTTTTLRTTT-----WSPGRSTTPSVSGR 462
Qy 320 IQPLSPQSPAPIASSPAIDMPPQSETISSPMPQTHVSGTPPPVKASFSS----- 368
Db 463 RNRSTSTP-----SPAIEVLNDI-----THVPSASQIPALESCAEVAREIMW 508
Qy 369 -----PTVSAPANVNT--TSAP-----PVQTDIVNTSSIDLENQVLMKALS 410
Db 509 FKTRGOMAKQPCPAGTIGVSTVLCIAPDGIWDQPGDLSNCS--SPVNHITQKLKS-- 564
Qy 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440
Db 565 -GETAANIARELAEOITRNHILNAGDITYSVRAMDQVLGLDVLQRLNLTGPKGDSAAARSLNK 623
Qy 441 -----AORLLKVVDDIGLQNFN-----TTISLTSPSLALAVIR-----VNAS 479
Db 624 LQKRSERAYVOAMVETVNNL--LQPALNAWRDLTSDQLRAATMLDITVEESAFVLAD 682
Qy 480 SNTTTFVAQDPANLOVSLAQENSGITITLPSL-----MNNLPAHDMELASR 530
Db 683 NLLKTDIVRENTDNIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLQKNGRGEIR 742
Qy 531 VQNFET--PALFQDPSLENLSL-----ISVSISSVANLTVRN-----LTR 571
Db 743 VAFVLYNNLGPYL-----STENASMKLGTEAMSTNHVSIVNTPVITAAINKFESNKVYLAD 798
Qy 572 NVTVTLKHINPQDELTVRCVFDLGRNGRGWGSDNGCSVKDRRLNETICTCSHLTSPG 631
Db 799 PVFTVKHKIKOSEENFNPCSWFSYKRTWTGYWSTQGCRLLTNTKHTTCSNHLTNFA 858
Qy 632 VLL----DLSTRSVLPQAMMALFTITVIGCGLSIFLSVTLVYIAFEKIRRDYPSKILIQ 688
Db 859 VLMAHVEVKHSDAV--HDLDDVITWVGILLSLVCLLICITFCFCFRGLQSD--RNTIHN 915
Qy 689 LCAALLNLNLVFL-----DSWIALYKMQGLCISVAVFLHVLVFTWGLFAHMYLA 743
Db 916 LCISLFAELLFLIGINRTDQPIA-----CAVFAALLHFFFLAAFTWMLFEGVQLYIM 968
Qy 744 LKVENT--YIRKYLKFCIVGMGVPVAVVITIIITISPDNKGGLSGYKGFPGSPDFQWI 801
Db 969 LVEPSEHSRRKY---FVLGVGMPALIVAVSAADVRSYG-----TDKVCWL 1014
Qy 802 NNAVYITVGVFCVIFLLNYSFMFIVLVOLCRICK--KQLGAQRKTSIQDLRSIAGL 859
Db 1015 RLDYVIFSWFISGTPATLIIMLVNIFGLIYALYKMFHHTAILKPESGCLDNKSWVIGAI--L 1073
Qy 860 TFLGITWGFAPFAGPVNVTFMYLFAINTLOGFTTFIFCYVAKENVRKOWRRYL--C 916
Db 1074 LCLGLTWAFGLMYNESIVIMAYLFTIFNSLOGMFIFHCVLQKKVRKEYGKCLRTHC 1133
Qy 917 C-----GKLRLENSDWSKATNGLKQKQVNOGVSSSSSLOSSS 956
Db 1134 CSGRSTESSIGSGKTSGRTPGRYSGSQSRIRRMWMDTVRKQSESSFITGDINSSASIN 1193
Qy 957 NSTSTLLVNDCSVHASN 977
Db 1194 RGAMANHLISNALLRPHGNN 1214

RESULT 19
O97824
ID O97824 PRELIMINARY; PRT: 1571 AA.
AC O97824;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LATROPHILIN 3 SPLICE VARIANT BBAF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=99148928; PubMed=10025961;
RA Matsushita H.; Lelianaova V.G.; Ushkaryov Y.A.;
RT "The latrophilin family: multiply spliced G protein-coupled receptors
RL with differential tissue distribution.";
FEBS Lett. 443:348-352(1999).
DR EMBL: AF111091; AAD05327.1; .
DR InterPro: IPR000922; Gal_lectin.
DR InterPro: IPR000832; GPCR_secretin.
DR InterPro: IPR001879; horrmn_receptor.
DR InterPro: IPR003334; Latrophilin.
DR InterPro: IPR003112; Olfac_like.
DR InterPro: IPR000203; PKD_cys_rich.
DR Pfam: PF00002; 7tm_2; 1.
DR Pfam: PF02140; Gal_lectin; 1.
DR Pfam: PF01825; GPS; 1.
DR Pfam: PF02793; HRM; 1.
DR Pfam: PF02354; Latrophilin; 1.
DR Pfam: PF02191; OLF; 1.
DR PRINTS: PR00249; GPCRSECRETIN.
DR PRODOM: PD005612; Gal_lectin; 1.
DR SMART: SM00303; GPS; 1.
DR SMART: SM00008; Hormr; 1.
DR SMART: SM00284; OLF; 1.
DR PROSITE: PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE: PS0261; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE: PS0228; SUEL_LECTIN; 1.
SQ SEQUENCE 1571 AA; 174901 MW; 2185D5ADCB5F8607 CRC64;

Query Match 10.0%; Score 534; DB 6; Length 1571;
Best Local Similarity 23.9%; Pred. No. 1e-28;
Matches 206; Conservative 124; Mismatches 333; Indels 198; Gaps 30;

Qy 260 LQDPIVCLADHPRGPPFSSQSIPVVRATVLSQVPKATSPAEPPDYSPVTHNVPSPIGE 319
Db 477 ISPIHLDSDLRPPVREISTGTGTLGTTTTLRTTT-----WSPGRSTTPSVSGR 530
Qy 320 IQPLSPQSPAPIASSPAIDMPPQSETISSPMPQTHVSGTPPPVKASFSS----- 368
Db 531 RNRSTSTP-----SPAIEVLNDI-----THVPSASQIPALESCAEVAREIMW 576
Qy 369 -----PTVSAPANVNT--TSAP-----PVQTDIVNTSSIDLENQVLMKALS 410
Db 577 FKTRGOMAKQPCPAGTIGVSTVLCIAPDGIWDQPGDLSNCS--SPVNHITQKLKS-- 632
Qy 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440
Db 633 -GETAANIARELAEOITRNHILNAGDITYSVRAMDQVLGLDVLQRLNLTGPKGDSAAARSLNK 691
Qy 441 -----AORLLKVVDDIGLQNFN-----TTISLTSPSLALAVIR-----VNAS 479
Db 692 LQKRSERAYVOAMVETVNNL--LQPALNAWRDLTSDQLRAATMLDITVEESAFVLAD 750
Qy 480 SNTTTFVAQDPANLOVSLAQENSGITITLPSL-----MNNLPAHDMELASR 530
Db 751 NLLKTDIVRENTDNIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLQKNGRGEIR 810
Qy 531 VQNFET--PALFQDPSLENLSL-----ISVSISSVANLTVRN-----LTR 571
Db 811 VAFVLYNNLGPYL-----STENASMKLGTEAMSTNHVSIVNTPVITAAINKFESNKVYLAD 866
Qy 572 NVTVTLKHINPQDELTVRCVFDLGRNGRGWGSDNGCSVKDRRLNETICTCSHLTSPG 631
Db 867 PVFTVKHKIKOSEENFNPCSWFSYKRTWTGYWSTQGCRLLTNTKHTTCSNHLTNFA 926
Qy 632 VLL----DLSTRSVLPQAMMALFTITVIGCGLSIFLSVTLVYIAFEKIRRDYPSKILIQ 688
Db 927 VLMAHVEVKHSDAV--HDLDDVITWVGILLSLVCLLICITFCFCFRGLQSD--RNTIHN 983
Qy 689 LCAALLNLNLVFL-----DSWIALYKMQGLCISVAVFLHVLVFTWGLFAHMYLA 743
Db 984 LCISLFAELLFLIGINRTDQPIA-----CAVFAALLHFFFLAAFTWMLFEGVQLYIM 1036


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QY 571 RNVTVTLKHINPSQDELTVRCVFWDLGRNGRGSGVCKDRRLNETICTCSHLTSP 630
D 210 DPVFTVKHIQSEENFNPCSEFWSKRTMTGYSTQGRLLTNTKTHTTCSCHLTNF 269
QY 631 GYLL---DLSRTSVLPQAMMALFITVIGGLSIFLSVTLVTVYAFKIRRDYPSKILI 687
D 270 AVLMAHVEVKHSDAV--HDLLODVITWGLLSLVCLLICITFCFFRGLQSD--RNTIHK 326
QY 688 QLCAALLLNMLVLL-----DSWTALYKMOGLCISVAVFLHYFLVSVFTWMLGLEAFHMYL 742
D 327 NLCISLFAVELLFLIGINRDTQPIA-----CAVEAALLHFFFLAFTWMPLEGVQLYI 379
QY 743 ALVKVNT--YIRKYILKFCIVGCVGPAVVVTVIILTISPNDYGLSGYKFPNGSPDDFCW 800
D 380 MLVEVFESHSRRKY---FVLVGYCMPALIVAVSAADYRSYG-----TDKVCW 425
QY 801 INNAVFIYTVGVFCVIFELNVSMFIVLVQLCRIKK--KKOLGAQRKTSIQDLRSIAG 858
D 426 LRDTYFIWFGIPATLIIMLVNIFGLYALKMHFTAILKPESCCLDNIKSWVICAIA- 484
QY 859 LTELGLITWGAFFAWGPNVNTFMFLFAINTLQOFFIFIFCYVAKENVKOW-----RRY 914
D 485 LLCLGLTWAGLWYINVESTVIMAYLFTIENSLOGMFIFHCVLQKKVKRKEYGKCLRTH 544
QY 915 LCCGKL-----RLAENS-----WSKTATNGLKKOTVNOGVSSSSNS 951
D 545 CCSGKSTESSIGSGKTSGRTPPGRYSTGSRIRRMWNT-----VRKQSESFITGDIN- 599
QY 952 LQSSNSTNSTLLVN--NDCSVHAS--GNGNASTERNGVSFSVQNGD 995
D 600 ---SSASLNREGLLNARDTSVMDTLPLNG-----HGNSYSIASGE 638

RESULT 23
O97810 PRELIMINARY; PRT: 1407 AA.
AC O97810
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE LATROPHILIN 2 SPLICED VARIANT BBAE.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148826; PubMed=10025961;
RA Matsushita H., Lellanova V.G., Ushkaryov Y.A.;
RT "The latrophilin family: multiply spliced G protein-coupled receptors
with differential tissue distribution.";
RL FEBS Lett. 443:348-352(1999).
DR EMBL; AF111077; AAD05313.1; -
DR InterPro; IPR000922; Gal.lectin.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR003334; Latrophilin.
DR InterPro; IPR003112; Olfac.-like.
DR InterPro; IPR00203; PKD_cys_rich.
DR InterPro; IPR002088; PPTA.
DR Pfam; PF00002; 7tm2.1.
DR Pfam; PF02140; Gal.Lectin; 1.
DR Pfam; PF01825; GPS; 1.
DR Pfam; PF02793; HRM; 1.
DR Pfam; PF02354; Latrophilin; 1.
DR Pfam; PF02191; OLF; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR ProDom; PD005612; Gal.lectin; 1.
DR SMART; SM00303; GPS; 1.
DR SMART; SM00008; Hornr; 1.
DR SMART; SM00284; OLF; 1.
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DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS00904; PPTA; UNKNOWN.1.
DR PROSITE; PS50228; SUEL.LECTIN; 1.
SQ SEQUENCE 1407 AA; 157657 MW; 01AF1591513D2C48 CRC64;

Query Match 9.9%; Score 531.5; DB 6; Length 1407;
Best Local Similarity 24.2%; Pred. No. 1.4e-28;
Matches 238; Conservative 161; Mismatches 422; Indels 225; Gaps 48;

QY 90 VETTSIND-----VTLSLPSN-----ETEKTIIVIKTFNAGVKPQR 128
D 188 IEYASLEDFQNSROTITTKLPNRVDGTGFVVYDVGAVFENKERT-NIVAYDLERIKSGE 246
QY 129 NICHNLSSICNDASFERG---EIMFOYDKES-----TVPONQIHITNGTLGVLSLSLEKRS 180
D 247 AIIINYAHDTSPYRWGKGKTDIDLAVDENGWLVIIVATEQN-----NGMVISQLNPY 298
QY 181 ELNKTLOTLSITYIMCATAEAQSTLNCTFTIKL-----NNTMNACAAIAALERVKIRPME 236
D 299 TLR--FEATWETVYDKRAASNAFMICGVLYVVRVYVDNESETGKNAIDYIYNTRLNRGE 356
QY 237 HCCSVIRIPCSSPEELKGLQCDLQDPIVCLADH-----PRGPP-----ES 277
D 357 Y----VDVFPFNQGYIAADVYNPRDNQLYVWNNFILRYSLSEFPGPPDPAQVPTTAVTIT 412
QY 278 SSQST---PVVPRATVLSQVPKATSAF-----EPPDYSPVTHNVPSPIGEIQPLS 324
D 413 SSAEMFKTVTSTTSOKGPMSTIVAGSQEGSKGTAKPAVSV--TTKIP-PVTNIEPL- 468
QY 325 PQSAPIASSPAIDMP-----POSE---TISPMPOTHVSGTPPPVKASFSPTVSAPANV 377
D 469 ----PERFCEALDARGIRWPOTQGMVMVERPCPK---GT-----RGTASYLCVL 510
QY 378 NTSAPPVQTDIVNTSS--ISDLENQVLQMEKALSIG-----SLEPNLAGEMINQVSR 429
D 511 STGTWNPKGPDLSNCTSHWNQLAQKIRSGENNAASLANELAKHTKGPVAGDVSSSV-RL 569
QY 430 LHSPPDML-APLAQRLLKVVDDIGIQLN--FSNTTISLTSPSLALAVIRVNAS--SFNTTT 485
D 570 MEQLVDILDAQLQELKPKSEKDSAGRSYNAKAVTDVNDLLRPEALESKHKMSSPQAHTAT 629
QY 486 -----FVAQDPANL---QVSLETO-----APENSIGTITLPSSLMN---- 518
D 630 MLLDTLEEGAFVYLD--NLVPEPTRVSMPTENIVLEVAVLSTEGQVQDFKPLGKAGSS 687
QY 519 -NLPADHMELASR--VOFNFTETPALFQDPSPLEN-----LSLSIYVISS 559
D 688 IQLSANTVKQNSRNGLAKLVFIYRSLGQFLSTENATIKLGADFIGRNSTIAVNSHVISV 747
QY 560 SYANLTVR-NLFRNVTVTLKHINPSQDELTVRCVFWDLGRNGRGSGVCKDRRLN 618
D 748 SINKESSRVYLDPVLTPLPHIDP-DNYFNANGSFNYSERTMGMYSSTQCKLVDTNKT 806
QY 619 ETICTCSHLTSGVLLDLSRTSVLP-AQMMALFTIYVIGGLSIFLSVTLVTVYAFKI 677
D 807 RTTCACSHLTNFALMAHREIAYKDGVHELLLVITWGIIVISLVCLAICITFCFFRGL 866
QY 678 RRDYPSKILIQLCALLLNVLFLDSWIALYKMOGLCISVAVFLHYFLVSVFTWMLGLEA 737
D 867 QSD-RNTIHKNLCLINFLIAEFILIG-IDTKYMIACPIFAGLLHFFFLAFAFAMWCLG 923
QY 738 FHMVYALVKVNT-YIRKYILKFCIVGCVGPAVVVTVIILTISPNDYGLSGYKFPNGSPD 796
D 924 VOLYLMLVEVFESEYSRKKY--YVAGYLEFPAIVVGSAAIDYKSYG-----TE 970
QY 797 DFCWINNAVFIYTVGVFCVIFELNVSMFIVLVQLCRIKKKQLGAQRKTSIQDLRS- 855
D 971 KACWLHVDNVIYFWSFIFGPVTFIILLNI---IFVITLCKWKVHNSLTKPDSRLNIKSW 1027
QY 856 IAG---LTELGLITWGAFFAWGPNVNTFMFLFAINTLQOFFIFIFCYVAKENVKOW- 911
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Db 1028 VLGAFAALLCLGLTWSFGLLFINETIVMAYLFTIFNAFGVFFIFPHCALQKVRKEYG 1087
QY 912 ---RYLCCGKL-----RLAENSWSKATNGLKKQTVNOGVSSSNSLQ 953
Db 1088 KCFRHSYCGGLFTSPSHSVKASTTFTSARYSSGTSQIRRMWNTVRKQSSSFISGD 1147
QY 954 SSSNSTNTTLLVNDSCVHAG-----NGNASTERNGVSFSVQNGD 995
Db 1148 INSTSTLNOGHSLLNARDTSAMDTLPLNGFNN-----SYSLRKG 1188
RESULT 24
Q92173 PRELIMINARY: PRT: 1550 AA.
ID Q92173
AC Q92173;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CALCIUM-INDEPENDENT ALPHA-LATROTOXIN RECEPTOR HOMOLOG 3.
GN CIRL-3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99150330; PubMed=10026162;
RA Ichtchenko K., Bittner M.A., Krasnoperov V., Little A.R., Chepurny O.,
RA Holz R.W., Petrenko A.G.;
RT "A novel ubiquitously expressed alpha-latrotoxin receptor is a member
RT of the CIRL family of G-protein-coupled receptors.";
RL J. Biol. Chem. 274:5491-5498(1999).
DR EMBL; AF063103; AAC7816.1; -
DR InterPro; IPR000922; Gal.lectin.
DR InterPro; IPR000832; GPCRsecretin.
DR InterPro; IPR001879; hormn.receptor.
DR InterPro; IPR003334; Latrophilin.
DR InterPro; IPR003112; Olfac.like.
DR InterPro; IPR000203; PKC_cys_rich.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02140; Gal.Lectin; 1.
DR Pfam; PF01825; GPS; 1.
DR Pfam; PF02793; HRM; 1.
DR Pfam; PF02354; Latrophilin; 1.
DR Pfam; PF02191; OLF; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRODOM; PD005612; Gal.lectin; 1.
DR SMART; SM00303; GPS; 1.
DR SMART; SM00008; Hormr; 1.
DR SMART; SM00284; OLF; 1.
DR PROSITE; PS50227; G-PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G-PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS50228; SUEL_LECTIN; 1.
KW Receptor.
SQ SEQUENCE 1550 AA; 172441 MW; A2E8091B2B34DB36 CRC64;

Query Match 9.9%; Score 531.5; DB 11; Length 1550;
Best Local Similarity 24.0%; Pred. No. 1.5e-28;
Matches 216; Conservative 135; Mismatches 347; Indels 203; Gaps 35;
QY 248 SSPELKLQCDLQDPVCLADHPGRGPPSSSGSIPVPRATVLSQVPKATSFAPPPDYS 307
Db 466 SGPVHGVQSVY-ISPPIHLSDLRPPVRGISTGTLGMSGSTTTTLRTTWNLGRSTT 524
QY 308 PV-----THNVPSPIGEIQLPSQPSAPIASSPAIDMPQSETISSPMPQTHVSGTTP 360
Db 525 PSLGRRNRSTSTPS- -AIEVLDVTHLPSSAASIPAMBEESCEAVEAREIMWPFKTRQG 582
QY 361 PVKASFSSPTVS-----APANVNTTSAPPVOTDVTNTSSISDLENQVLMKALSLGS 413
Db 583 VAKOSCPAGTIGVSYLCLAPDGPQGP-----DLNSCS--SPWNHITQKLKS---GE 633

QY 414 LEPNLAGEMINOVSRLLHS-----PPDMLAPL----- 440
Db 634 TAANIARELAETRNHLNAGDITYSVRAMDQVLGDLVQLRNLTGPGKDSAAARSLNKLOK 693
QY 441 -----AORLLKVVDDIGLQNFNS-----TTISLTPSLALAVIR-----VNASSFN 482
Db 694 RERSCRAYVQAMVETVNNL-LQPALNAWRDLTTSQDLRAATMLLDTVEESAFVLADNLL 752
QY 483 TTFVFAQDPANLOVSLQAPENSIGTITLPPSL-----MNNLPAHDMELASRVQF 533
Db 753 KTDIVRENTDNIQLEVARLSTEGNLEDLKPFGTGHSTIQLSANTLKONGRNGEIRVAF 812
QY 534 NEFET--PALFQDPSLENLSL-----ISYVISSVANLTVRN-----LTRNVT 574
Db 813 VLYNNGPVL-----STENASMKLGTEAMSTNHSIVNSPVITAAINKEFSNKVYLADPV 868
QY 575 VTLKIINQSODELTVRVCVFDLGRNGRGWSDGSCVKDRRLNETICTCSHLTSGVLL 634
Db 869 FTVKHIKQSEENFPNCSFWSYSKRTMTGYWSTQGCRLTNTKTHTTCSNHLTNFAVILM 928
QY 635 ---DLRSRTSVLPAQMMAALFTVTYIGCGLSSTIFLSVTLVTYIAFEKIRRDYPSKILLQLCA 691
Db 929 AHVEVKHSDAV--HDLLEDVITWVGILLVCLLICITFTCFRGLQSD--RNTIHKNLCI 995
QY 692 ALLLLNLVFL-----DSWIALYKMOGLCISAVFLHYFLVSVFTWGLGAFHMYLALVK 746
Db 986 SLFVAELLFLIGINRDTQPIA-----CAVFAALLHFFELAAFTWMLFEGVQLYIMLVE 1038
QY 747 VENT--YIRKYILKFCIVGWGPVAVVTIILTISPNDYGLSGYKFPNGSPDPDFCWINNN 804
Db 1039 VFSEHSRRKY---FYLGVGMPALIVAVSAADVRSYG-----TDKVCWLRLD 1084
QY 805 AVEYITVVGYFCVIFLLNVSMFTVLVOLCRICK--KKOLGAQRKTSIODLR----- 854
Db 1085 TYFHSFGPATLIIMLVIFGLIALYKMFHHTAILPESCLDNINEDNRPFTKSWYI 1144
QY 855 SIAGTLFLGITWGAFFAWGPVNVTFMYLFAINTLQGFIFIFYCYVAKENVRKQW--- 911
Db 1145 GAIALCLLGLTWAFLMYINESTVIMAYLFTIFNSLQGMFEIFHCVLQKVRKEYGKC 1204
QY 912 -RRYLCCGKL-----RLAENS-----WSKTATNGLKKTQVNOGVSS 947
Db 1205 LRTHCCSGKSTESSGSGKTSRTPGRTGSGSRIRRMWNT-----VRKQSSSFITG 1260
QY 948 SSNSLQSSNSTNSTL-----LVNN--DCSVHAS--GNGNASTERNGVSFSVQNG 994
Db 1261 DINSSASLNRGSLYLCIQACVTVYLEGLLNARDTSVMDTLPLNGN-----HGNSYSIAGG 1315
QY 995 D 995
Db 1316 E 1316
RESULT 25
O97819 PRELIMINARY: PRT: 1231 AA.
ID O97819
AC O97819;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE LATROPHILIN 3 SPLICE VARIANT ABAG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9914828; PubMed=10025961;
RA Matsushita H., Lelanova V.G., Ushkaryov Y.A.;
RT "The latrophilin family: multiply spliced G protein-coupled receptors
RT with differential tissue distribution.";
RL FEBS Lett. 443:348-352(1999).

